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(54) Title: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER			
(57) Abstract Compounds and methods for the treatment and diagnosis of lung cancer are provided. The inventive compounds include polypeptides containing at least a portion of a lung tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of lung cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.			

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COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER

TECHNICAL FIELD

5 The present invention relates generally to therapy and diagnosis of cancer, such as lung cancer. The invention is more specifically related to polypeptides comprising at least a portion of a lung tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of lung cancer, and for the
10 diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

 Lung cancer is the primary cause of cancer death among both men and women in the U.S., with an estimated 172,000 new cases being reported in 1994. The five-year survival rate among all lung cancer patients, regardless of the stage of disease
15 at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among cases detected while the disease is still localized. However, only 16% of lung cancers are discovered before the disease has spread.

 Early detection is difficult since clinical symptoms are often not seen until the disease has reached an advanced stage. Currently, diagnosis is aided by the
20 use of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic examination of the bronchial passages. Treatment regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. In spite of considerable research into therapies for the disease, lung cancer remains difficult to treat.

25 Accordingly, there remains a need in the art for improved vaccines, treatment methods and diagnostic techniques for lung cancer.

SUMMARY OF THE INVENTION

 Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as lung cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a lung tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347 and 349; (b) variants of a sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347 and 349; and (c) complements of a sequence of (a) or (b). In specific embodiments, the polypeptides of the present invention comprise at least a portion of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 152, 155, 156, 165, 166, 169, 170, 172, 174, 176, 226-252, 338-344 and 346, and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a lung tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a lung tumor protein; and (b) a physiologically acceptable carrier.

5 Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

10 Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above, and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

15 Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

20 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

25 The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

30 Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Determined T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells determined from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a lung tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be lung cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the

sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

5

SEQUENCE IDENTIFIERS

- SEQ ID NO: 1 is the determined cDNA sequence for LST-S1-2
SEQ ID NO: 2 is the determined cDNA sequence for LST-S1-28
SEQ ID NO: 3 is the determined cDNA sequence for LST-S1-90
10 SEQ ID NO: 4 is the determined cDNA sequence for LST-S1-144
SEQ ID NO: 5 is the determined cDNA sequence for LST-S1-133
SEQ ID NO: 6 is the determined cDNA sequence for LST-S1-169
SEQ ID NO: 7 is the determined cDNA sequence for LST-S2-6
SEQ ID NO: 8 is the determined cDNA sequence for LST-S2-11
15 SEQ ID NO: 9 is the determined cDNA sequence for LST-S2-17
SEQ ID NO: 10 is the determined cDNA sequence for LST-S2-25
SEQ ID NO: 11 is the determined cDNA sequence for LST-S2-39
SEQ ID NO: 12 is a first determined cDNA sequence for LST-S2-43
SEQ ID NO: 13 is a second determined cDNA sequence for LST-S2-43
20 SEQ ID NO: 14 is the determined cDNA sequence for LST-S2-65
SEQ ID NO: 15 is the determined cDNA sequence for LST-S2-68
SEQ ID NO: 16 is the determined cDNA sequence for LST-S2-72
SEQ ID NO: 17 is the determined cDNA sequence for LST-S2-74
SEQ ID NO: 18 is the determined cDNA sequence for LST-S2-103
25 SEQ ID NO: 19 is the determined cDNA sequence for LST-S2-N1-1F
SEQ ID NO: 20 is the determined cDNA sequence for LST-S2-N1-2A
SEQ ID NO: 21 is the determined cDNA sequence for LST-S2-N1-4H
SEQ ID NO: 22 is the determined cDNA sequence for LST-S2-N1-5A
SEQ ID NO: 23 is the determined cDNA sequence for LST-S2-N1-6B
30 SEQ ID NO: 24 is the determined cDNA sequence for LST-S2-N1-7B
SEQ ID NO: 25 is the determined cDNA sequence for LST-S2-N1-7H

- SEQ ID NO: 26 is the determined cDNA sequence for LST-S2-N1-8A
SEQ ID NO: 27 is the determined cDNA sequence for LST-S2-N1-8D
SEQ ID NO: 28 is the determined cDNA sequence for LST-S2-N1-9A
SEQ ID NO: 29 is the determined cDNA sequence for LST-S2-N1-9E
5 SEQ ID NO: 30 is the determined cDNA sequence for LST-S2-N1-10A
SEQ ID NO: 31 is the determined cDNA sequence for LST-S2-N1-10G
SEQ ID NO: 32 is the determined cDNA sequence for LST-S2-N1-11A
SEQ ID NO: 33 is the determined cDNA sequence for LST-S2-N1-12C
SEQ ID NO: 34 is the determined cDNA sequence for LST-S2-N1-12E
10 SEQ ID NO: 35 is the determined cDNA sequence for LST-S2-B1-3D
SEQ ID NO: 36 is the determined cDNA sequence for LST-S2-B1-6C
SEQ ID NO: 37 is the determined cDNA sequence for LST-S2-B1-5D
SEQ ID NO: 38 is the determined cDNA sequence for LST-S2-B1-5F
SEQ ID NO: 39 is the determined cDNA sequence for LST-S2-B1-6G
15 SEQ ID NO: 40 is the determined cDNA sequence for LST-S2-B1-8A
SEQ ID NO: 41 is the determined cDNA sequence for LST-S2-B1-8D
SEQ ID NO: 42 is the determined cDNA sequence for LST-S2-B1-10A
SEQ ID NO: 43 is the determined cDNA sequence for LST-S2-B1-9B
SEQ ID NO: 44 is the determined cDNA sequence for LST-S2-B1-9F
20 SEQ ID NO: 45 is the determined cDNA sequence for LST-S2-B1-12D
SEQ ID NO: 46 is the determined cDNA sequence for LST-S2-I2-2B
SEQ ID NO: 47 is the determined cDNA sequence for LST-S2-I2-5F
SEQ ID NO: 48 is the determined cDNA sequence for LST-S2-I2-6B
SEQ ID NO: 49 is the determined cDNA sequence for LST-S2-I2-7F
25 SEQ ID NO: 50 is the determined cDNA sequence for LST-S2-I2-8G
SEQ ID NO: 51 is the determined cDNA sequence for LST-S2-I2-9E
SEQ ID NO: 52 is the determined cDNA sequence for LST-S2-I2-12B
SEQ ID NO: 53 is the determined cDNA sequence for LST-S2-H2-2C
SEQ ID NO: 54 is the determined cDNA sequence for LST-S2-H2-1G
30 SEQ ID NO: 55 is the determined cDNA sequence for LST-S2-H2-4G
SEQ ID NO: 56 is the determined cDNA sequence for LST-S2-H2-3H

- SEQ ID NO: 57 is the determined cDNA sequence for LST-S2-H2-5G
SEQ ID NO: 58 is the determined cDNA sequence for LST-S2-H2-9B
SEQ ID NO: 59 is the determined cDNA sequence for LST-S2-H2-10H
SEQ ID NO: 60 is the determined cDNA sequence for LST-S2-H2-12D
5 SEQ ID NO: 61 is the determined cDNA sequence for LST-S3-2
SEQ ID NO: 62 is the determined cDNA sequence for LST-S3-4
SEQ ID NO: 63 is the determined cDNA sequence for LST-S3-7
SEQ ID NO: 64 is the determined cDNA sequence for LST-S3-8
SEQ ID NO: 65 is the determined cDNA sequence for LST-S3-12
10 SEQ ID NO: 66 is the determined cDNA sequence for LST-S3-13
SEQ ID NO: 67 is the determined cDNA sequence for LST-S3-14
SEQ ID NO: 68 is the determined cDNA sequence for LST-S3-16
SEQ ID NO: 69 is the determined cDNA sequence for LST-S3-21
SEQ ID NO: 70 is the determined cDNA sequence for LST-S3-22
15 SEQ ID NO: 71 is the determined cDNA sequence for LST-S1-7
SEQ ID NO: 72 is the determined cDNA sequence for LST-S1-A-1E
SEQ ID NO: 73 is the determined cDNA sequence for LST-S1-A-1G
SEQ ID NO: 74 is the determined cDNA sequence for LST-S1-A-3E
SEQ ID NO: 75 is the determined cDNA sequence for LST-S1-A-4E
20 SEQ ID NO: 76 is the determined cDNA sequence for LST-S1-A-6D
SEQ ID NO: 77 is the determined cDNA sequence for LST-S1-A-8D
SEQ ID NO: 78 is the determined cDNA sequence for LST-S1-A-10A
SEQ ID NO: 79 is the determined cDNA sequence for LST-S1-A-10C
SEQ ID NO: 80 is the determined cDNA sequence for LST-S1-A-9D
25 SEQ ID NO: 81 is the determined cDNA sequence for LST-S1-A-10D
SEQ ID NO: 82 is the determined cDNA sequence for LST-S1-A-9H
SEQ ID NO: 83 is the determined cDNA sequence for LST-S1-A-11D
SEQ ID NO: 84 is the determined cDNA sequence for LST-S1-A-12D
SEQ ID NO: 85 is the determined cDNA sequence for LST-S1-A-11E
30 SEQ ID NO: 86 is the determined cDNA sequence for LST-S1-A-12E
SEQ ID NO: 87 is the determined cDNA sequence for L513S (T3).

- SEQ ID NO: 88 is the determined cDNA sequence for L513S contig 1.
- SEQ ID NO: 89 is a first determined cDNA sequence for L514S.
- SEQ ID NO: 90 is a second determined cDNA sequence for L514S.
- SEQ ID NO: 91 is a first determined cDNA sequence for L516S.
- 5 SEQ ID NO: 92 is a second determined cDNA sequence for L516S.
- SEQ ID NO: 93 is the determined cDNA sequence for L517S.
- SEQ ID NO: 94 is the extended cDNA sequence for LST-S1-169 (also known as L519S).
- SEQ ID NO: 95 is a first determined cDNA sequence for L520S.
- 10 SEQ ID NO: 96 is a second determined cDNA sequence for L520S.
- SEQ ID NO: 97 is a first determined cDNA sequence for L521S.
- SEQ ID NO: 98 is a second determined cDNA sequence for L521S.
- SEQ ID NO: 99 is the determined cDNA sequence for L522S.
- SEQ ID NO: 100 is the determined cDNA sequence for L523S.
- 15 SEQ ID NO: 101 is the determined cDNA sequence for L524S.
- SEQ ID NO: 102 is the determined cDNA sequence for L525S.
- SEQ ID NO: 103 is the determined cDNA sequence for L526S.
- SEQ ID NO: 104 is the determined cDNA sequence for L527S.
- SEQ ID NO: 105 is the determined cDNA sequence for L528S.
- 20 SEQ ID NO: 106 is the determined cDNA sequence for L529S.
- SEQ ID NO: 107 is a first determined cDNA sequence for L530S.
- SEQ ID NO: 108 is a second determined cDNA sequence for L530S.
- SEQ ID NO: 109 is the determined full-length cDNA sequence for L531S short form
- SEQ ID NO: 110 is the predicted amino acid sequence encoded by SEQ ID NO: 109.
- 25 SEQ ID NO: 111 is the determined full-length cDNA sequence for L531S long form
- SEQ ID NO: 112 is the predicted amino acid sequence encoded by SEQ ID NO: 111.
- SEQ ID NO: 113 is the determined full-length cDNA sequence for L520S.
- SEQ ID NO: 114 is the predicted amino acid sequence encoded by SEQ ID NO: 113.
- SEQ ID NO: 115 is the determined cDNA sequence for contig 1.
- 30 SEQ ID NO: 116 is the determined cDNA sequence for contig 3.
- SEQ ID NO: 117 is the determined cDNA sequence for contig 4.

- SEQ ID NO: 118 is the determined cDNA sequence for contig 5.
- SEQ ID NO: 119 is the determined cDNA sequence for contig 7.
- SEQ ID NO: 120 is the determined cDNA sequence for contig 8.
- SEQ ID NO: 121 is the determined cDNA sequence for contig 9.
- 5 SEQ ID NO: 122 is the determined cDNA sequence for contig 10.
- SEQ ID NO: 123 is the determined cDNA sequence for contig 12.
- SEQ ID NO: 124 is the determined cDNA sequence for contig 11.
- SEQ ID NO: 125 is the determined cDNA sequence for contig 13.
- SEQ ID NO: 126 is the determined cDNA sequence for contig 15.
- 10 SEQ ID NO: 127 is the determined cDNA sequence for contig 16.
- SEQ ID NO: 128 is the determined cDNA sequence for contig 17.
- SEQ ID NO: 129 is the determined cDNA sequence for contig 19.
- SEQ ID NO: 130 is the determined cDNA sequence for contig 20.
- SEQ ID NO: 131 is the determined cDNA sequence for contig 22.
- 15 SEQ ID NO: 132 is the determined cDNA sequence for contig 24.
- SEQ ID NO: 133 is the determined cDNA sequence for contig 29.
- SEQ ID NO: 134 is the determined cDNA sequence for contig 31.
- SEQ ID NO: 135 is the determined cDNA sequence for contig 33.
- SEQ ID NO: 136 is the determined cDNA sequence for contig 38.
- 20 SEQ ID NO: 137 is the determined cDNA sequence for contig 39.
- SEQ ID NO: 138 is the determined cDNA sequence for contig 41.
- SEQ ID NO: 139 is the determined cDNA sequence for contig 43.
- SEQ ID NO: 140 is the determined cDNA sequence for contig 44.
- SEQ ID NO: 141 is the determined cDNA sequence for contig 45.
- 25 SEQ ID NO: 142 is the determined cDNA sequence for contig 47.
- SEQ ID NO: 143 is the determined cDNA sequence for contig 48.
- SEQ ID NO: 144 is the determined cDNA sequence for contig 49.
- SEQ ID NO: 145 is the determined cDNA sequence for contig 50.
- SEQ ID NO: 146 is the determined cDNA sequence for contig 53.
- 30 SEQ ID NO: 147 is the determined cDNA sequence for contig 54.
- SEQ ID NO: 148 is the determined cDNA sequence for contig 56.

- SEQ ID NO: 149 is the determined cDNA sequence for contig 57.
- SEQ ID NO: 150 is the determined cDNA sequence for contig 58.
- SEQ ID NO: 151 is the full-length cDNA sequence for L530S.
- SEQ ID NO: 152 is the amino acid sequence encoded by SEQ ID NO: 151
- 5 SEQ ID NO: 153 is the full-length cDNA sequence of a first variant of L514S
- SEQ ID NO: 154 is the full-length cDNA sequence of a second variant of L514S
- SEQ ID NO: 155 is the amino acid sequence encoded by SEQ ID NO: 153.
- SEQ ID NO: 156 is the amino acid sequence encoded by SEQ ID NO: 154.
- SEQ ID NO: 157 is the determined cDNA sequence for contig 59.
- 10 SEQ ID NO: 158 is the full-length cDNA sequence for L763P (also referred to as contig 22).
- SEQ ID NO: 159 is the amino acid sequence encoded by SEQ ID NO: 158.
- SEQ ID NO: 160 is the full-length cDNA sequence for L762P (also referred to as contig 17).
- 15 SEQ ID NO: 161 is the amino acid sequence encoded by SEQ ID NO: 160.
- SEQ ID NO: 162 is the determined cDNA sequence for L515S.
- SEQ ID NO: 163 is the full-length cDNA sequence of a first variant of L524S.
- SEQ ID NO: 164 is the full-length cDNA sequence of a second variant of L524S.
- SEQ ID NO: 165 is the amino acid sequence encoded by SEQ ID NO: 163.
- 20 SEQ ID NO: 166 is the amino acid sequence encoded by SEQ ID NO: 164.
- SEQ ID NO: 167 is the full-length cDNA sequence of a first variant of L762P.
- SEQ ID NO: 168 is the full-length cDNA sequence of a second variant of L762P.
- SEQ ID NO: 169 is the amino acid sequence encoded by SEQ ID NO: 167.
- SEQ ID NO: 170 is the amino acid sequence encoded by SEQ ID NO: 168.
- 25 SEQ ID NO: 171 is the full-length cDNA sequence for L773P (also referred to as contig 56).
- SEQ ID NO: 172 is the amino acid sequence encoded by SEQ ID NO: 171.
- SEQ ID NO: 173 is an extended cDNA sequence for L519S.
- SEQ ID NO: 174 is the predicted amino acid sequence encoded by SEQ ID NO: 174.
- 30 SEQ ID NO: 175 is the full-length cDNA sequence for L523S.
- SEQ ID NO: 176 is the predicted amino acid sequence encoded by SEQ ID NO: 175.

- SEQ ID NO: 177 is the determined cDNA sequence for LST-sub5-7A.
SEQ ID NO: 178 is the determined cDNA sequence for LST-sub5-8G.
SEQ ID NO: 179 is the determined cDNA sequence for LST-sub5-8H.
SEQ ID NO: 180 is the determined cDNA sequence for LST-sub5-10B.
5 SEQ ID NO: 181 is the determined cDNA sequence for LST-sub5-10H.
SEQ ID NO: 182 is the determined cDNA sequence for LST-sub5-12B.
SEQ ID NO: 183 is the determined cDNA sequence for LST-sub5-11C.
SEQ ID NO: 184 is the determined cDNA sequence for LST-sub6-1c.
SEQ ID NO: 185 is the determined cDNA sequence for LST-sub6-2f.
10 SEQ ID NO: 186 is the determined cDNA sequence for LST-sub6-2G.
SEQ ID NO: 187 is the determined cDNA sequence for LST-sub6-4d.
SEQ ID NO: 188 is the determined cDNA sequence for LST-sub6-4e.
SEQ ID NO: 189 is the determined cDNA sequence for LST-sub6-4f.
SEQ ID NO: 190 is the determined cDNA sequence for LST-sub6-3h.
15 SEQ ID NO: 191 is the determined cDNA sequence for LST-sub6-5d.
SEQ ID NO: 192 is the determined cDNA sequence for LST-sub6-5h.
SEQ ID NO: 193 is the determined cDNA sequence for LST-sub6-6h.
SEQ ID NO: 194 is the determined cDNA sequence for LST-sub6-7a.
SEQ ID NO: 195 is the determined cDNA sequence for LST-sub6-8a.
20 SEQ ID NO: 196 is the determined cDNA sequence for LST-sub6-7d.
SEQ ID NO: 197 is the determined cDNA sequence for LST-sub6-7e.
SEQ ID NO: 198 is the determined cDNA sequence for LST-sub6-8e.
SEQ ID NO: 199 is the determined cDNA sequence for LST-sub6-7g.
SEQ ID NO: 200 is the determined cDNA sequence for LST-sub6-9f.
25 SEQ ID NO: 201 is the determined cDNA sequence for LST-sub6-9h.
SEQ ID NO: 202 is the determined cDNA sequence for LST-sub6-11b.
SEQ ID NO: 203 is the determined cDNA sequence for LST-sub6-11c.
SEQ ID NO: 204 is the determined cDNA sequence for LST-sub6-12c.
SEQ ID NO: 205 is the determined cDNA sequence for LST-sub6-12e.
30 SEQ ID NO: 206 is the determined cDNA sequence for LST-sub6-12f.
SEQ ID NO: 207 is the determined cDNA sequence for LST-sub6-11g.

- SEQ ID NO: 208 is the determined cDNA sequence for LST-sub6-12g.
SEQ ID NO: 209 is the determined cDNA sequence for LST-sub6-12h.
SEQ ID NO: 210 is the determined cDNA sequence for LST-sub6-II-1a.
SEQ ID NO: 211 is the determined cDNA sequence for LST-sub6-II-2b.
5 SEQ ID NO: 212 is the determined cDNA sequence for LST-sub6-II-2g.
SEQ ID NO: 213 is the determined cDNA sequence for LST-sub6-II-1h.
SEQ ID NO: 214 is the determined cDNA sequence for LST-sub6-II-4a.
SEQ ID NO: 215 is the determined cDNA sequence for LST-sub6-II-4b.
SEQ ID NO: 216 is the determined cDNA sequence for LST-sub6-II-3e.
10 SEQ ID NO: 217 is the determined cDNA sequence for LST-sub6-II-4f.
SEQ ID NO: 218 is the determined cDNA sequence for LST-sub6-II-4g.
SEQ ID NO: 219 is the determined cDNA sequence for LST-sub6-II-4h.
SEQ ID NO: 220 is the determined cDNA sequence for LST-sub6-II-5c.
SEQ ID NO: 221 is the determined cDNA sequence for LST-sub6-II-5e.
15 SEQ ID NO: 222 is the determined cDNA sequence for LST-sub6-II-6f.
SEQ ID NO: 223 is the determined cDNA sequence for LST-sub6-II-5g.
SEQ ID NO: 224 is the determined cDNA sequence for LST-sub6-II-6g.
SEQ ID NO: 225 is the amino acid sequence for L528S.
SEQ ID NO: 226-251 are synthetic peptides derived from L762P.
20 SEQ ID NO: 252 is the expressed amino acid sequence of L514S.
SEQ ID NO: 253 is the DNA sequence corresponding to SEQ ID NO: 252.
SEQ ID NO: 254 is the DNA sequence of a L762P expression construct.
SEQ ID NO: 255 is the determined cDNA sequence for clone 23785.
SEQ ID NO: 256 is the determined cDNA sequence for clone 23786.
25 SEQ ID NO: 257 is the determined cDNA sequence for clone 23788.
SEQ ID NO: 258 is the determined cDNA sequence for clone 23790.
SEQ ID NO: 259 is the determined cDNA sequence for clone 23793.
SEQ ID NO: 260 is the determined cDNA sequence for clone 23794.
SEQ ID NO: 261 is the determined cDNA sequence for clone 23795.
30 SEQ ID NO: 262 is the determined cDNA sequence for clone 23796.
SEQ ID NO: 263 is the determined cDNA sequence for clone 23797.

- SEQ ID NO: 264 is the determined cDNA sequence for clone 23798.
SEQ ID NO: 265 is the determined cDNA sequence for clone 23799.
SEQ ID NO: 266 is the determined cDNA sequence for clone 23800.
SEQ ID NO: 267 is the determined cDNA sequence for clone 23802.
5 SEQ ID NO: 268 is the determined cDNA sequence for clone 23803.
SEQ ID NO: 269 is the determined cDNA sequence for clone 23804.
SEQ ID NO: 270 is the determined cDNA sequence for clone 23805.
SEQ ID NO: 271 is the determined cDNA sequence for clone 23806.
SEQ ID NO: 272 is the determined cDNA sequence for clone 23807.
10 SEQ ID NO: 273 is the determined cDNA sequence for clone 23808.
SEQ ID NO: 274 is the determined cDNA sequence for clone 23809.
SEQ ID NO: 275 is the determined cDNA sequence for clone 23810.
SEQ ID NO: 276 is the determined cDNA sequence for clone 23811.
SEQ ID NO: 277 is the determined cDNA sequence for clone 23812.
15 SEQ ID NO: 278 is the determined cDNA sequence for clone 23813.
SEQ ID NO: 279 is the determined cDNA sequence for clone 23815.
SEQ ID NO: 280 is the determined cDNA sequence for clone 25298.
SEQ ID NO: 281 is the determined cDNA sequence for clone 25299.
SEQ ID NO: 282 is the determined cDNA sequence for clone 25300.
20 SEQ ID NO: 283 is the determined cDNA sequence for clone 25301
SEQ ID NO: 284 is the determined cDNA sequence for clone 25304
SEQ ID NO: 285 is the determined cDNA sequence for clone 25309.
SEQ ID NO: 286 is the determined cDNA sequence for clone 25312.
SEQ ID NO: 287 is the determined cDNA sequence for clone 25317.
25 SEQ ID NO: 288 is the determined cDNA sequence for clone 25321.
SEQ ID NO: 289 is the determined cDNA sequence for clone 25323.
SEQ ID NO: 290 is the determined cDNA sequence for clone 25327.
SEQ ID NO: 291 is the determined cDNA sequence for clone 25328.
SEQ ID NO: 292 is the determined cDNA sequence for clone 25332.
30 SEQ ID NO: 293 is the determined cDNA sequence for clone 25333.
SEQ ID NO: 294 is the determined cDNA sequence for clone 25336.

- SEQ ID NO: 295 is the determined cDNA sequence for clone 25340.
SEQ ID NO: 296 is the determined cDNA sequence for clone 25342.
SEQ ID NO: 297 is the determined cDNA sequence for clone 25356.
SEQ ID NO: 298 is the determined cDNA sequence for clone 25357.
5 SEQ ID NO: 299 is the determined cDNA sequence for clone 25361.
SEQ ID NO: 300 is the determined cDNA sequence for clone 25363.
SEQ ID NO: 301 is the determined cDNA sequence for clone 25397.
SEQ ID NO: 302 is the determined cDNA sequence for clone 25402.
SEQ ID NO: 303 is the determined cDNA sequence for clone 25403.
10 SEQ ID NO: 304 is the determined cDNA sequence for clone 25405.
SEQ ID NO: 305 is the determined cDNA sequence for clone 25407.
SEQ ID NO: 306 is the determined cDNA sequence for clone 25409.
SEQ ID NO: 307 is the determined cDNA sequence for clone 25396.
SEQ ID NO: 308 is the determined cDNA sequence for clone 25414.
15 SEQ ID NO: 309 is the determined cDNA sequence for clone 25410.
SEQ ID NO: 310 is the determined cDNA sequence for clone 25406.
SEQ ID NO: 311 is the determined cDNA sequence for clone 25306.
SEQ ID NO: 312 is the determined cDNA sequence for clone 25362.
SEQ ID NO: 313 is the determined cDNA sequence for clone 25360.
20 SEQ ID NO: 314 is the determined cDNA sequence for clone 25398.
SEQ ID NO: 315 is the determined cDNA sequence for clone 25355.
SEQ ID NO: 316 is the determined cDNA sequence for clone 25351.
SEQ ID NO: 317 is the determined cDNA sequence for clone 25331.
SEQ ID NO: 318 is the determined cDNA sequence for clone 25338.
25 SEQ ID NO: 319 is the determined cDNA sequence for clone 25335.
SEQ ID NO: 320 is the determined cDNA sequence for clone 25329.
SEQ ID NO: 321 is the determined cDNA sequence for clone 25324.
SEQ ID NO: 322 is the determined cDNA sequence for clone 25322.
SEQ ID NO: 323 is the determined cDNA sequence for clone 25319.
30 SEQ ID NO: 324 is the determined cDNA sequence for clone 25316.
SEQ ID NO: 325 is the determined cDNA sequence for clone 25311.

- SEQ ID NO: 326 is the determined cDNA sequence for clone 25310.
SEQ ID NO: 327 is the determined cDNA sequence for clone 25302.
SEQ ID NO: 328 is the determined cDNA sequence for clone 25315.
SEQ ID NO: 329 is the determined cDNA sequence for clone 25308.
5 SEQ ID NO: 330 is the determined cDNA sequence for clone 25303.
SEQ ID NO: 331-337 are the cDNA sequences of isoforms of the p53 tumor suppressor
homologue, p63 (also referred to as L530S).
SEQ ID NO: 338-344 are the amino acid sequences encoded by SEQ ID NO: 331-337,
respectively.
10 SEQ ID NO: 345 is a second cDNA sequence for the antigen L763P.
SEQ ID NO: 346 is the amino acid sequence encoded by the sequence of SEQ ID NO:
345.
SEQ ID NO: 347 is a determined full-length cDNA sequence for L523S.
SEQ ID NO: 348 is the predicted amino acid sequence encoded by SEQ ID NO: 347.
15 SEQ ID NO: 349 is the cDNA sequence encoding the N-terminal portion of L773P.
SEQ ID NO: 350 is the amino acid sequence of the N-terminal portion of L773P.

DETAILED DESCRIPTION OF THE INVENTION

- As noted above, the present invention is generally directed to
20 compositions and methods for the therapy and diagnosis of cancer, such as lung cancer.
The compositions described herein may include lung tumor polypeptides,
polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen
presenting cells (APCs) and/or immune system cells (e.g., T cells). Polypeptides of the
present invention generally comprise at least a portion (such as an immunogenic
25 portion) of a lung tumor protein or a variant thereof. A "lung tumor protein" is a protein
that is expressed in lung tumor cells at a level that is at least two fold, and preferably at
least five fold, greater than the level of expression in a normal tissue, as determined
using a representative assay provided herein. Certain lung tumor proteins are tumor
proteins that react detectably (within an immunoassay, such as an ELISA or Western
30 blot) with antisera of a patient afflicted with lung cancer. Polynucleotides of the subject
invention generally comprise a DNA or RNA sequence that encodes all or a portion of

such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery human lung tumor proteins. Sequences of polynucleotides encoding specific tumor proteins are provided in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349.

LUNG TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a lung tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a lung tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a lung tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a lung tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the

encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide
5 sequence that encodes a native lung tumor protein or a portion thereof. The term “variants” also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be “identical” if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two
10 sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A “comparison window” as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences
15 are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A
20 model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989)
25 *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

30 Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20

positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native lung tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (i.e., expression that

is at least two fold greater in a lung tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and
5 Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as lung tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

10 An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a lung tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be
15 preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured
20 bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using
25 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be
30 generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs

may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding portions of lung tumor proteins are provided in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a lung tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a lung tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription

initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled
5 with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*.
10 Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

15 Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation
20 vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to
25 permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not
30 limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus).). The polynucleotides may also be administered as naked

plasmid vectors. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

15 LUNG TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a lung tumor protein or a variant thereof, as described herein. As noted above, a "lung tumor protein" is a protein that is expressed by lung tumor cells. Proteins that are lung tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with lung cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a lung tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may

contain a small N- and/or C-terminal deletion (e.g., 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (i.e., they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native lung tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native lung tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native lung tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include

those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

5 Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the

polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above
5 may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host
10 cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or
15 more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example,
20 such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems
25 Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known
30 tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans,

or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second

polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements
5 responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the
10 present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is
15 derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred
20 embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different
25 fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292,
30 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible

for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see 5 *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides 10 as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is 15 considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and 20 antigen-binding fragments thereof, that specifically bind to a lung tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a lung tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a lung tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association 25 between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding 30 constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a lung tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.

Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest
5 may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as
10 described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid
15 cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

20 Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by
25 conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be
30 prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,

Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or
5 more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria
10 toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a
15 substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an
20 antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents,
25 which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups,
30 sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody
5 used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a lung tumor protein. Such cells may generally be prepared *in vitro* or
10 *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO
15 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a lung tumor polypeptide, polynucleotide encoding a lung tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a
20 time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a lung tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a lung tumor polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the
25 polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et
30 al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell

proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a lung tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a lung tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Lung tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a lung tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a lung tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a lung tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a lung tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant

may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl.*

Acad. Sci. USA 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 5 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier 10 will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. 15 For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres 20 are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) 25 and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a 30 substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A,

Bordetella pertussis or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA);
5 aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

10 Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the
15 induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using
20 standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt.
25 MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT) (see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences
30 are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc.,

Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with
5 cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France),
10 SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Ribi ImmunoChem Research Inc., Hamilton, MT), RC-529 (Ribi ImmunoChem Research Inc., Hamilton, MT) and Aminoalkyl glucosaminide 4-phosphates (AGPs).

15 Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound
20 following administration). Such formulations may generally be prepared using well known technology (*see, e.g.* Coombes et al., *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained
25 within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-
30 release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally,

an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood,

bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a lung tumor protein (or portion or other variant thereof) such that the lung tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein.

Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the lung tumor polypeptide, DNA

(naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as lung cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive

long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free

survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a lung tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent

that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the

binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at
5 A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody.
10 Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

15 More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to
20 bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of
25 that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

30 Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second

antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide.

5 An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are
10 generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of
15 the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average
20 mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical*
25 *Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that
30 encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered

positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

5 In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution
10 containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent.
15 Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the
20 biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about
25 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to
30 those of ordinary skill in the art that the above protocols may be readily modified to use lung tumor polypeptides to detect antibodies that bind to such polypeptides in a

biological sample. The detection of such lung tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a lung tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a lung tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of lung tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a lung tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a lung tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the lung tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a lung tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%,

preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a lung tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed
5 herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a
10 sequence recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

15 One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification
20 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered
25 positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be
30 performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the

level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor.

- 5 One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

- 10 As noted above, to improve sensitivity, multiple lung tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins
15 provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

- The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components
20 necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a lung tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements,
25 such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

- Alternatively, a kit may be designed to detect the level of mRNA encoding a lung tumor protein in a biological sample. Such kits generally comprise at
30 least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a lung tumor protein. Such an oligonucleotide may be used,

for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a lung tumor protein.

The following Examples are offered by way of illustration and not by
5 way of limitation.

EXAMPLE 1
ISOLATION AND CHARACTERIZATION OF cDNA SEQUENCES
ENCODING LUNG TUMOR POLYPEPTIDES

5

This example illustrates the isolation of cDNA molecules encoding lung tumor-specific polypeptides from lung tumor cDNA libraries.

A. ISOLATION OF cDNA SEQUENCES FROM A LUNG SQUAMOUS CELL
10 CARCINOMA LIBRARY

A human lung squamous cell carcinoma cDNA expression library was constructed from poly A⁺ RNA from a pool of two patient tissues using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD) following the manufacturer's protocol. Specifically, lung carcinoma
15 tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using an oligo dT cellulose column as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. First-strand cDNA was
20 synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with BstXI/EcoRI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with cDNA size fractionation columns (BRL Life Technologies), the cDNA was ligated into the BstXI/NotI site of pcDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life
25 Technologies) by electroporation.

Using the same procedure, a normal human lung cDNA expression library was prepared from a pool of four tissue specimens. The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The lung
30 squamous cell carcinoma library contained 2.7×10^6 independent colonies, with 100% of clones having an insert and the average insert size being 2100 base pairs. The normal

lung cDNA library contained 1.4×10^6 independent colonies, with 90% of clones having inserts and the average insert size being 1800 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA

5 cDNA library subtraction was performed using the above lung squamous cell carcinoma and normal lung cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a lung squamous cell carcinoma-specific subtracted cDNA library was generated as follows. Normal tissue cDNA library (80 μ g) was digested with BamHI and XhoI, followed by a filling-in
10 reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 133 μ l of H₂O, heat-denatured and mixed with 133 μ l (133 μ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (67 μ l) was added
15 and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μ l H₂O to form the driver DNA.

To form the tracer DNA, 10 μ g lung squamous cell carcinoma cDNA library was digested with NotI and SpeI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech, Palo Alto, CA). Typically, 5 μ g of
20 cDNA was recovered after the sizing column. Following ethanol precipitation, the tracer DNA was dissolved in 5 μ l H₂O. Tracer DNA was mixed with 15 μ l driver DNA and 20 μ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and
25 incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μ l H₂O, mixed with 8 μ l driver DNA and 20 μ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After
30 removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into NotI/SpeI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA) and

transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a lung squamous cell carcinoma specific subtracted cDNA library (herein after referred to as "lung subtraction I").

5 A second lung squamous cell carcinoma specific subtracted cDNA library (referred to as "lung subtraction II") was generated in a similar way to the lung subtraction library I, except that eight frequently recovered genes from lung subtraction I were included in the driver DNA, and 24,000 independent clones were recovered.

To analyze the subtracted cDNA libraries, plasmid DNA was prepared from 320 independent clones, randomly picked from the subtracted lung squamous cell carcinoma specific libraries. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A and/or Model 377 (Foster City, CA). The cDNA sequences for sixty isolated clones are provided in SEQ ID NO: 1-60. These sequences were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). No significant homologies were found to the sequences provided in SEQ ID NO: 2, 3, 19, 38 and 46. The sequences of SEQ ID NO: 1, 6-8, 10-13, 15, 17, 18, 20-27, 29, 30, 32, 34-37, 39-45, 47-49, 51, 52, 54, 55 and 57-59 were found to show some homology to previously identified expressed sequence tags (ESTs). The sequences of SEQ ID NO: 9, 28, 31 and 33 were found to show some homology to previously identified non-human gene sequences and the sequences of SEQ ID NO: 4, 5, 14, 50, 53, 56 and 60 were found to show some homology to gene sequences previously identified in humans.

The subtraction procedure described above was repeated using the above lung squamous cell carcinoma cDNA library as the tracer DNA, and the above normal lung tissue cDNA library and a cDNA library from normal liver and heart (constructed from a pool of one sample of each tissue as described above), plus twenty other cDNA clones that were frequently recovered in lung subtractions I and II, as the driver DNA (lung subtraction III). The normal liver and heart cDNA library contained 1.76×10^6 independent colonies, with 100% of clones having inserts and the average insert size being 1600 base pairs. Ten additional clones were isolated (SEQ ID NO: 61-70). Comparison of these cDNA sequences with those in the gene bank as described above,

revealed no significant homologies to the sequences provided in SEQ ID NO: 62 and 67. The sequences of SEQ ID NO: 61, 63-66, 68 and 69 were found to show some homology to previously isolated ESTs and the sequence provided in SEQ ID NO: 70 was found to show some homology to a previously identified rat gene.

5 In further studies, the subtraction procedure described above was repeated using the above lung squamous cell carcinoma cDNA library as the tracer DNA, and a cDNA library from a pool of normal lung, kidney, colon, pancreas, brain, resting PBMC, heart, skin and esophagus as the driver DNA, with esophagus cDNAs making up one third of the driver material. Since esophagus is enriched in normal
10 epithelial cells, including differentiated squamous cells, this procedure is likely to enrich genes that are tumor specific rather than tissues specific. The cDNA sequences of 48 clones determined in this subtraction are provided in SEQ ID NO: 177-224. The sequences of SEQ ID NO: 177, 178, 180, 181, 183, 187, 192, 195-197, 208, 211, 212, 215, 216, 218 and 219 showed some homology to previously identified genes. The
15 sequences of SEQ ID NO: 179, 182, 184-186, 188-191, 193, 194, 198-207, 209 210, 213, 214, 217, 220 and 224 showed some homology to previously determined ESTs. The sequence of SEQ ID NO: 221-223 showed no homology to any previously determined sequence.

20 B. ISOLATION OF cDNA SEQUENCES FROM A LUNG ADENOCARCINOMA LIBRARY

A human lung adenocarcinoma cDNA expression library was constructed as described above. The library contained 3.2×10^6 independent colonies, with 100% of clones having an insert and the average insert size being 1500 base pairs.
25 Library subtraction was performed as described above using the normal lung and normal liver and heart cDNA expression libraries described above as the driver DNA. Twenty-six hundred independent clones were recovered.

Initial cDNA sequence analysis from 100 independent clones revealed many ribosomal protein genes. The cDNA sequences for fifteen clones isolated in this
30 subtraction are provided in SEQ ID NO: 71-86. Comparison of these sequences with those in the gene bank as described above revealed no significant homologies to the

sequence provided in SEQ ID NO: 84. The sequences of SEQ ID NO: 71, 73, 74, 77, 78 and 80-82 were found to show some homology to previously isolated ESTs, and the sequences of SEQ ID NO: 72, 75, 76, 79, 83 and 85 were found to show some homology to previously identified human genes.

5 In further studies, a cDNA library (referred to as mets3616A) was constructed from a metastatic lung adenocarcinoma. The determined cDNA sequences of 25 clones sequenced at random from this library are provided in SEQ ID NO: 255-279. The mets3616A cDNA library was subtracted against a cDNA library prepared from a pool of normal lung, liver, pancreas, skin, kidney, brain and resting PBMC. To
10 increase the specificity of the subtraction, the driver was spiked with genes that were determined to be most abundant in the mets3616A cDNA library, such as EF1-alpha, integrin-beta and anticoagulant protein PP4, as well as with cDNAs that were previously found to be differentially expressed in subtracted lung adenocarcinoma cDNA libraries. The determined cDNA sequences of 51 clones isolated from the
15 subtracted library (referred to as mets3616A-S1) are provided in SEQ ID NO: 280-330.

Comparison of the sequences of SEQ ID NO: 255-330 with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 255-258, 260, 262-264, 270, 272, 275, 276, 279, 281, 287, 291, 296, 300 and 310. The sequences of SEQ ID NO: 259, 261, 265-269, 271, 273, 274, 277, 278, 282-285, 288-
20 290, 292, 294, 297-299, 301, 303-309, 313, 314, 316, 320-324 and 326-330 showed some homology to previously identified gene sequences, while the sequences of SEQ ID NO: 280, 286, 293, 302, 310, 312, 315, 317-319 and 325 showed some homology to previously isolated expressed sequence tags (ESTs).

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EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF LUNG TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for seven
30 representative lung tumor polypeptides described in Example 1 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. 1 μ l of 1:30 dilution of cDNA was employed to enable the linear range amplification of the β -actin template and was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in five different types of tumor tissue (lung squamous cell carcinoma from 3 patients, lung adenocarcinoma, colon tumor from 2 patients, breast tumor and prostate tumor), and thirteen different normal tissues (lung from 4 donors, prostate, brain, kidney, liver, ovary, skeletal muscle, skin, small intestine, stomach, myocardium, retina and testes). Using a 10-fold amount of cDNA, the antigen LST-S1-90 (SEQ ID NO: 3) was found to be expressed at high levels in lung squamous cell carcinoma and in breast tumor, and at low to undetectable levels in the other tissues examined.

The antigen LST-S2-68 (SEQ ID NO: 15) appears to be specific to lung and breast tumor, however, expression was also detected in normal kidney. Antigens LST-S1-169 (SEQ ID NO: 6) and LST-S1-133 (SEQ ID NO: 5) appear to be very abundant in lung tissues (both normal and tumor), with the expression of these two genes being decreased in most of the normal tissues tested. Both LST-S1-169 and LST-S1-133 were also expressed in breast and colon tumors. Antigens LST-S1-6 (SEQ ID NO: 7) and LST-S2-I2-5F (SEQ ID NO: 47) did not show tumor or tissue specific expression, with the expression of LST-S1-28 being rare and only detectable in a few tissues. The antigen LST-S3-7 (SEQ ID NO: 63) showed lung and breast tumor specific expression, with its message only being detected in normal testes when the PCR was performed for 30 cycles. Lower level expression was detected in some

normal tissues when the cycle number was increased to 35. Antigen LST-S3-13 (SEQ ID NO: 66) was found to be expressed in 3 out of 4 lung tumors, one breast tumor and both colon tumor samples. Its expression in normal tissues was lower compared to tumors, and was only detected in 1 out of 4 normal lung tissues and in normal tissues
5 from kidney, ovary and retina. Expression of antigens LST-S3-4 (SEQ ID NO: 62) and LST-S3-14 (SEQ ID NO: 67) was rare and did not show any tissue or tumor specificity. Consistent with Northern blot analyses, the RT-PCT results on antigen LAT-S1-A-10A (SEQ ID NO: 78) suggested that its expression is high in lung, colon, stomach and small intestine tissues, including lung and colon tumors, whereas its expression was low
10 or undetectable in other tissues.

A total of 2002 cDNA fragments isolated in lung subtractions I, II and III, described above, were colony PCR amplified and their mRNA expression levels in lung tumor, normal lung, and various other normal and tumor tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification
15 products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization
20 intensity. Seventeen non-redundant cDNA clones showed over-expression in lung squamous tumors, with expression in normal tissues tested (lung, skin, lymph node, colon, liver, pancreas, breast, heart, bone marrow, large intestine, kidney, stomach, brain, small intestine, bladder and salivary gland) being either undetectable, or 10-fold less compared to lung squamous tumors. The determined partial cDNA sequences for
25 the clone L513S are provided in SEQ ID NO: 87 and 88; those for L514S are provided in SEQ ID NO: 89 and 90; those for L516S in SEQ ID NO: 91 and 92; that for L517S in SEQ ID NO: 93; that for L519S in SEQ ID NO: 94; those for L520S in SEQ ID NO: 95 and 96; those for L521S in SEQ ID NO: 97 and 98; that for L522S in SEQ ID NO: 99; that for L523S in SEQ ID NO: 100; that for L524S in SEQ ID NO: 101; that for
30 L525S in SEQ ID NO: 102; that for L526S in SEQ ID NO: 103; that for L527S in SEQ ID NO: 104; that for L528S in SEQ ID NO: 105; that for L529S in SEQ ID NO: 106;

and those for L530S in SEQ ID NO: 107 and 108. Additionally, the full-length cDNA sequence for L530S is provided in SEQ ID NO: 151, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 152. L530S shows homology to a splice variant of a p53 tumor suppressor homologue, p63. The cDNA sequences of 7
5 known isoforms of p63 are provided in SEQ ID NO: 331-337, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 338-344, respectively.

Due to polymorphisms, the clone L531S appears to have two forms. A first determined full-length cDNA sequence for L531S is provided in SEQ ID NO: 109, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:
10 110. A second determined full-length cDNA sequence for L531S is provided in SEQ ID NO: 111, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 112. The sequence of SEQ ID NO: 111 is identical to that of SEQ ID NO: 109, except that it contains a 27 bp insertion. Similarly, L514S also has two alternatively spliced forms; the first variant cDNA is listed as SEQ ID NO: 153, with
15 the corresponding amino acid sequence being provided in SEQ ID NO: 155. The second variant form of L514S full-length cDNA is provided in SEQ ID NO: 154, with its corresponding amino acid sequence being provided in SEQ ID NO: 156.

Full length cloning for L524S (SEQ ID NO: 101) yielded two variants (SEQ ID NO: 163 and 164) with the corresponding predicted amino acid sequences of
20 SEQ ID NO: 165 and 166, respectively. Both variants have been shown to encode parathyroid hormone-related peptide.

Attempts to isolate the full-length cDNA for L519S, resulted in the isolation of the extended cDNA sequence provided in SEQ ID NO: 173, which contains a potential open reading frame. The predicted amino acid sequence encoded by the
25 sequence of SEQ ID NO: 173 is provided in SEQ ID NO: 174. Additionally, the full-length cDNA sequence for the clone of SEQ ID NO: 100 (known as L523S), a known gene, is provided in SEQ ID NO: 175, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 176. In further studies, a full-length cDNA sequence for L523S was isolated from a L523S-positive tumor cDNA library by PCR
30 amplification using gene specific primers designed from the sequence of SEQ ID NO: 175. The determined cDNA sequence is provided in SEQ ID NO: **. The amino acid

sequence encoded by this sequence is provided in SEQ ID NO: **. This protein sequence differs from the previously published protein sequence at two amino acid positions, namely at positions 158 and 410.

Comparison of the sequences of L514S and L531S (SEQ ID NO: 87 and 88, 89 and 90, and 109, respectively) with those in the gene bank, as described above, revealed no significant homologies to known sequences. The sequences of L513S, L516S, L517S, L519S, L520S and L530S (SEQ ID NO: 87 and 88, 91 and 92, 93, 94, 95 and 96, 107 and 108, respectively) were found to show some homology to previously identified ESTs. The sequences of L521S, L522S, L523S, L524S, L525S, L526S, L527S, L528S and L529S (SEQ ID NO: 97 and 98, 99, 99, 101, 102, 103, 104, 105, and 106, respectively) were found to represent known genes. The determined full-length cDNA sequences for L520S is provided in SEQ ID NO: 113, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 114. Subsequent microarray analysis has shown L520S to be overexpressed in breast tumors in addition to lung squamous tumors.

Further analysis has demonstrated that L529S (SEQ ID NO: 106 and 115), L525S (SEQ ID NO: 102 and 120) and L527S (SEQ ID NO: 104) are cytoskeletal components and potentially squamous cell specific proteins. L529S is connexin 26, a gap junction protein. It is highly expressed in lung squamous tumor 9688T, and moderately over-expressed in two others. However, lower level expression of connexin 26 is also detectable in normal skin, colon, liver and stomach. The over-expression of connexin 26 in some breast tumors has been reported and a mutated form of L529S may result in over-expression in lung tumors. L525S is plakophilin 1, a desmosomal protein found in plaque-bearing adhering junctions of the skin. Expression levels for L525S mRNA is highly elevated in three out of four lung squamous tumors tested, and in normal skin. L527S has been identified as keratin 6 isoform, type II 58 Kd keratin, and cytokeratin 13 and shows over-expression in squamous tumors and low expression in normal skin, breast and colon tissues. Notably, keratin and keratin-related genes have been extensively documented as potential markers for lung cancer including CYFRA2.1 (Pastor, A., et al, *Eur. Respir. J.*, 10:603-609, 1997). L513S (SEQ ID NO: 87 and 88)

shows moderate over-expression in several tumor tissues tested, and encodes a protein that was first isolated as a pemphigus vulgaris antigen.

L520S (SEQ ID NO: 95 and 96) and L521S (SEQ ID NO: 97 and 98) are highly expressed in lung squamous tumors, and L520S is up-regulated in normal salivary gland and L521S is over-expressed in normal skin. Both belong to a family of small proline rich proteins and represent markers for fully differentiated squamous cells. L521S has been described as a specific marker for lung squamous tumor (Hu, R., et al, *Lung Cancer*, 20:25-30, 1998). L515S (SEQ ID NO: 162) encodes IGF- β 2 and L516S is an aldose reductase homologue and both are moderately expressed in lung squamous tumors and in normal colon. Notably, L516S (SEQ ID NO: 91 and 92) is up-regulated in metastatic tumors but not primary lung adenocarcinoma, an indication of its potential role in metatasis and a potential prognostic marker. L522S (SEQ ID NO: 99) is moderately over-expressed in lung squamous tumors with minimum expression in normal tissues. L522S has been shown to belong to a class IV alcohol dehydrogenase, ADH7, and its expression profile suggests it is a squamous cell specific antigen. L523S (SEQ ID NO: 100) is moderately over-expressed in lung squamous tumor, human pancreatic cancer cell lines and pancreatic cancer tissues, suggesting this gene may be a shared antigen between pancreatic and lung squamous cell cancer.

L524S (SEQ ID NO: 101) is over-expressed in the majority of squamous tumors tested and is homologous with parathyroid hormone-related peptide (PTHrP), which is best known to cause humoral hypercalcaemia associated with malignant tumors such as leukemia, prostate and breast cancer. It is also believed that PTHrP is most commonly associated with squamous carcinoma of lung and rarely with lung adenocarcinoma (Davidson, L.A., et al, *J. Pathol.*, 178: 398-401, 1996). L528S (SEQ ID NO: 105) is highly over-expressed in two lung squamous tumors with moderate expression in two other squamous tumors, one lung adenocarcinoma and some normal tissues, including skin, lymph nodes, heart, stomach and lung. It encodes the NMB gene that is similar to the precursor of melanocyte specific gene Pmel17, which is reported to be preferentially expressed in low-metastatic potential melanoma cell lines. This suggests that L528S may be a shared antigen in both melanoma and lung squamous cell carcinoma. L526S (SEQ ID NO: 103) is overexpressed in all lung

squamous cell tumor tissues tested and has been shown to share homology with a gene (ATM) in which a mutation causes ataxia telangiectasia, a genetic disorder in humans causing a predisposition to cancer, among other symptoms. ATM encodes a protein that activates p53 mediated cell-cycle checkpoint through direct binding and phosphorylation of the p53 molecule. Approximately 40% of lung cancer is associated with p53 mutations, and it is speculated that over-expression of ATM is a result of compensation for loss of p53 function, but it is unknown whether over-expression is the cause of result of lung squamous cell carcinoma. Additionally, expression of L526S (ATM) is also detected in a metastatic but not lung adenocarcinoma, suggesting a role in metastasis.

Expression of L523S (SEQ ID NO: 175), was also examined by real time RT-PCR as described above. In a first study using a panel of lung squamous tumors, L523S was found to be expressed in 4/7 lung squamous tumors, 2/3 head and neck squamous tumors and 2/2 lung adenocarcinomas, with low level expression being observed in skeletal muscle, soft palate and tonsil. In a second study using a lung adenocarcinoma panel, expression of L523S was observed in 4/9 primary adenocarcinomas, 2/2 lung pleural effusions, 1/1 metastatic lung adenocarcinomas and 2/2 lung squamous tumors, with little expression being observed in normal tissues.

Expression of L523S in lung tumors and various normal tissues was also examined by Northern blot analysis, using standard techniques. In a first study, L523S was found to be expressed in a number of lung adenocarcinomas and squamous cell carcinomas, as well as normal tonsil. No expression was observed in normal lung. In a second study using a normal tissue blot (HB-12) from Clontech, no expression was observed in brain, skeletal muscle, colon, thymus, spleen, kidney, liver, small intestine, lung or PBMC, although there was strong expression in placenta.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF LUNG TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

Eight hundred and fifty seven clones from a cDNA subtraction library, containing cDNA from a pool of two human lung squamous tumors subtracted against eight normal human tissue cDNAs including lung, PBMC, brain, heart, kidney, liver, pancreas, and skin, (Clontech, Palo Alto, CA) were derived and submitted to a first round of PCR amplification. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector P7- Adv vector (Clontech, Palo Alto, CA) and transformed into DH5 α *E. coli* (Gibco, BRL). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

One hundred and sixty two positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the the EMBL and GenBank databases, as described above, revealed no significant homologies to 13 of these clones, hereinafter referred to as Contigs 13, 16, 17, 19, 22, 24, 29, 47, 49, 56-59. The determined cDNA sequences for these clones are provided in SEQ ID NO: 125, 127-129, 131-133, 142, 144, 148-150, and 157, respectively. Contigs 1, 3-5, 7-10, 12, 11, 15, 20, 31, 33, 38, 39, 41, 43, 44, 45, 48, 50, 53, 54 (SEQ ID NO: 115-124, 126, 130, 134-141, 143, 145-147, respectively) were found to show some degree of homology to previously identified DNA sequences. Contig 57 (SEQ ID NO: 149) was found to represent the clone L519S (SEQ ID NO: 94) disclosed in US. Patent Application No. 09/123,912, filed July 27, 1998. To the best of the inventors' knowledge, none of these sequences have been previously shown to be differentially over-expressed in lung tumors.

mRNA expression levels for representative clones in lung tumor tissues, normal lung tissues (n=4), resting PBMC, salivary gland, heart, stomach, lymph nodes, skeletal muscle, soft palate, small intestine, large intestine, bronchial, bladder, tonsil, kidney, esophagus, bone marrow, colon, adrenal gland, pancreas, and skin, (all derived from human) were determined by RT-PCR as described above. Expression levels using microarray technology, as described above, were examined in one sample of each tissue type unless otherwise indicated.

Contig 3 (SEQ ID NO: 116) was found to be highly expressed in all head and neck squamous cell tumors tested (17/17), and expressed in the majority (8/12) of lung squamous tumors, (high expression in 7/12, moderate in 2/12, and low in 2/12), while showing negative expression for 2/4 normal lung tissues and low expression in the remaining two samples. Contig 3 showed moderate expression in skin and soft palate, and lowered expression levels in resting PBMC, large intestine, salivary gland, tonsil, pancreas, esophagus, and colon. Contig 11 (SEQ ID NO: 124) was found to be expressed in all head and neck squamous cell tumors tested (17/17): highly expressed in 14/17, and moderately expressed in 3/17. Additionally, expression in lung squamous tumors showed high expression in 3/12 and moderate in 4/12. Contig 11 was negative for 3/4 normal lung samples, with the remaining sample having only low expression. Contig 11 showed low to moderate reactivity to salivary gland, soft palate, bladder, tonsil, skin, esophagus, and large intestine. Contig 13 (SEQ ID NO: 125) was found to be expressed in all head and neck squamous cell tumors tested (17/17): highly expressed in 12/17, and moderately expressed in 5/17. Contig 13 was expressed in 7/12 lung squamous tumors, with high expression in 4/12 and moderate expression in three samples. Analysis of normal lung samples showed negative expression for 2/4 and low to moderate expression in the remaining two samples. Contig 13 did show low to moderate reactivity to resting PBMC, salivary gland, bladder, pancreas, tonsil, skin, esophagus, and large intestine, as well as high expression in soft palate. Contig 16 (SEQ ID NO: 127) was found to be moderately expressed in some head and neck squamous cell tumors (6/17) and one lung squamous tumor; while showing no expression in any normal lung samples tested. Contig 16 did show low reactivity to resting PBMC, large intestine, skin, salivary gland, and soft palate. Contig 17 (SEQ ID NO: 128) was shown to be expressed in all head and neck squamous cell tumors tested (17/17): highly expressed in 5/17, and moderately expressed in 12/17. Expression levels in lung squamous tumors showed one tumor sample with high expression and 3/12 with moderate levels. Contig 17 was negative for 2/4 normal lung samples, with the remaining samples having only low expression. Additionally, low level expression was found in esophagus and soft palate. Contig 19 (SEQ ID NO: 129) was found to be expressed in most head and neck squamous cell tumors tested (11/17); with two

samples having high levels, 6/17 showing moderate expression, and low expression being found in 3/17. Testing in lung squamous tumors revealed only moderate expression in 3/12 samples. Expression levels in 2/4 of normal lung samples were negative, the two other samples having only low expression. Contig 19 showed low expression levels in esophagus, resting PBMC, salivary gland, bladder, soft palate and pancreas.

Contig 22 (SEQ ID NO: 131), was shown to be expressed in most head and neck squamous cell tumors tested (13/17) with high expression in four of these samples, moderate expression in 6/17, and low expression in 3/17. Expression levels in lung squamous tumors were found to be moderate to high for 3/12 tissues tested, with negative expression in two normal lung samples and low expression in two other samples (n=4). Contig 22 showed low expression in skin, salivary gland and soft palate. Similarly, Contig 24 (SEQ ID NO: 132) was found to be expressed in most head and neck squamous cell tumors tested (13/17) with high expression in three of these samples, moderate expression in 6/17, and low expression in 4/17. Expression levels in lung squamous tumors were found to be moderate to high for 3/12 tissues tested, with negative expression for three normal lung samples and low expression in one sample (n=4). Contig 24 showed low expression in skin, salivary gland and soft palate. Contig 29 (SEQ ID NO: 133) was expressed in nearly all head and neck squamous cell tumors tested (16/17): highly expressed in 4/17, moderately expressed in 11/17, with low expression in one sample. Also, it was moderately expressed in 3/12 lung squamous tumors, while being negative for 2/4 normal lung samples. Contig 29 showed low to moderate expression in large intestine, skin, salivary gland, pancreas, tonsil, heart and soft palate. Contig 47 (SEQ ID NO: 142) was expressed in most head and neck squamous cell tumors tested (12/17): moderate expression in 10/17, and low expression in two samples. In lung squamous tumors, it was highly expressed in one sample and moderately expressed in two others (n=13). Contig 47 was negative for 2/4 normal lung samples, with the remaining two samples having moderate expression. Also, Contig 47 showed moderate expression in large intestine, and pancreas, and low expression in skin, salivary gland, soft palate, stomach, bladder, resting PBMC, and tonsil.

Contig 48 (SEQ ID NO: 143) was expressed in all head and neck squamous cell tumors tested (17/17): highly expressed in 8/17 and moderately expressed in 7/17, with low expression in two samples. Expression levels in lung squamous tumors were high to moderate in three samples (n=13). Contig 48 was negative for one out of four normal lung samples, the remaining showing low or moderate expression. Contig 48 showed moderate expression in soft palate, large intestine, pancreas, and bladder, and low expression in esophagus, salivary gland, resting PBMC, and heart. Contig 49 (SEQ ID NO: 144) was expressed at low to moderate levels in 6/17 head and neck squamous cell tumors tested. Expression levels in lung squamous tumors were moderate in three samples (n=13). Contig 49 was negative for 2/4 normal lung samples, the remaining samples showing low expression. Moderate expression levels in skin, salivary gland, large intestine, pancreas, bladder and resting PBMC were shown, as well as low expression in soft palate, lymph nodes, and tonsil. Contig 56 (SEQ ID NO: 148) was expressed in low to moderate levels in 3/17 head and neck squamous cell tumors tested, and in lung squamous tumors, showing low to moderate levels in three out of thirteen samples. Notably, low expression levels were detected in one adenocarcinoma lung tumor sample (n=2). Contig 56 was negative for 3/4 normal lung samples, and showed moderate expression levels in only large intestine, and low expression in salivary gland, soft palate, pancreas, bladder, and resting PBMC. Contig 58, also known as L769P, (SEQ ID NO: 150) was expressed at moderate levels in 11/17 head and neck squamous cell tumors tested and low expression in one additional sample. Expression in lung squamous tumors showed low to moderate levels in three out of thirteen samples. Contig 58 was negative for 3/4 normal lung samples, with one sample having low expression. Moderate expression levels in skin, large intestine, and resting PBMC were demonstrated, as well as low expression in salivary gland, soft palate, pancreas, and bladder. Contig 59 (SEQ ID NO: 157) was expressed in some head, neck, and lung squamous tumors. Low level expression of Contig 59 was also detected in salivary gland and large intestine.

The full-length cDNA sequence for Contig 22, also referred to as L763P, is provided in SEQ ID NO: 158, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 159. Real-time RT-PCR analysis of L763P revealed

that it is highly expressed in 3/4 lung squamous tumors as well as 4/4 head and neck squamous tumors, with low level expression being observed in normal brain, skin, soft pallet and trachea. Subsequent database searches revealed that the sequence of SEQ ID NO: 158 contains a mutation, resulting in a frameshift in the corresponding protein sequence. A second cDNA sequence for L763P is provided in SEQ ID NO: 345, with the corresponding amino acid sequence being provided in SEQ ID NO: 346. The sequences of SEQ ID NO: 159 and 346 are identical with the exception of the C-terminal 33 amino acids of SEQ ID NO: 159.

The full-length cDNA sequence incorporating Contigs 17, 19, and 24, referred to as L762P, is provided in SEQ ID NO: 160, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 161. Further analysis of L762P has determined it to be a type I membrane protein and two additional variants have been sequenced. Variant 1 (SEQ ID NO: 167, with the corresponding amino acid sequence in SEQ ID NO: 169) is an alternatively spliced form of SEQ ID NO: 160 resulting in deletion of 503 nucleotides, as well as deletion of a short segment of the expressed protein. Variant 2 (SEQ ID NO: 168, with the corresponding amino acid sequence in SEQ ID NO: 170) has a two nucleotide deletion at the 3' coding region in comparison to SEQ ID NO: 160, resulting in a secreted form of the expressed protein. Real-time RT-PCR analysis of L762P revealed that is over-expressed in 3/4 lung squamous tumors and 4/4 head & neck tumors, with low level expression being observed in normal skin, soft pallet and trachea.

The full-length cDNA sequence for contig 56 (SEQ ID NO: 148), also referred to as L773P, is provided in SEQ ID NO: 171, with the predicted amino acid sequence in SEQ ID NO: 172. L773P was found to be identical to dihydroxyl dehydrogenase at the 3' portion of the gene, with divergent 5' sequence. As a result, the 69 N-terminal amino acids are unique. The cDNA sequence encoding the 69 N-terminal amino acids is provided in SEQ ID NO: 349, with the N-terminal amino acid sequence being provided in SEQ ID NO: 350. Real-time PCR revealed that L773P is highly expressed in lung squamous tumor and lung adenocarcinoma, with no detectable expression in normal tissues. Subsequent Northern blot analysis of L773P demonstrated that this transcript is differentially over-expressed in squamous tumors

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and detected at approximately 1.6 Kb in primary lung tumor tissue and approximately 1.3 Kb in primary head and neck tumor tissue.

Subsequent microarray analysis has shown Contig 58, also referred to as L769S (SEQ ID NO: 150), to be overexpressed in breast tumors in addition to lung
5 squamous tumors.

EXAMPLE 4 SYNTHESIS OF POLYPEPTIDES

10 Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide.
15 Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse
20 phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

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EXAMPLE 5

PREPARATION OF ANTIBODIES AGAINST LUNG CANCER ANTIGENS

Polyclonal antibodies against the lung cancer antigens L514S, L528S and L531S (SEQ ID NO: 155, 225 and 112, respectively) were prepared as follows.

30

Rabbits were immunized with recombinant protein expressed in and purified from *E. coli* as described above. For the initial immunization, 400 µg of

antigen combined with muramyl dipeptide (MDP) was injected subcutaneously (S.C.). Animals were boosted S.C. 4 weeks later with 200 µg of antigen mixed with incomplete Freund's Adjuvant (IFA). Subsequent boosts of 100 µg of antigen mixed with IFA were injected S.C. as necessary to induce high antibody titer responses. Serum bleeds
5 from immunized rabbits were tested for antigen-specific reactivity using ELISA assays with purified protein. Polyclonal antibodies against L514S, L528S and L531S were affinity purified from high titer polyclonal sera using purified protein attached to a solid support.

Immunohistochemical analysis using polyclonal antibodies against
10 L514S was performed on a panel of 5 lung tumor samples, 5 normal lung tissue samples and normal colon, kidney, liver, brain and bone marrow. Specifically, tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with antibody for 1 hr. HRP-labeled anti-mouse followed by incubation with DAB
15 chromogen was used to visualize L514S immunoreactivity. L514S was found to be highly expressed in lung tumor tissue with little or no expression being observed in normal lung, brain or bone marrow. Light staining was observed in colon and kidney. Staining was seen in normal liver but no mRNA has been detected in this tissue making this result suspect.

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EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

Immunogenic peptides from the lung cancer antigen L762P (SEQ ID
25 NO: 161) for HLA-A2/K^b-restricted CD8⁺ T cells were identified as follows.

The location of HLA-A2 binding peptides within the lung cancer antigen L762P (SEQ ID NO: 161) was predicted using a computer program which predicts peptides sequences likely to be to HLA-A*0201 by fitting to the known peptide binding motif for HLA-A*0201 (Rupert *et al.* (1993) *Cell* 74:929; Rammensee *et al.*
30 (1995) *Immunogenetics* 41:178-228). A series of 19 synthetic peptides corresponding to a selected subset of the predicted HLA-A*0201 binding peptides was prepared as described above.

Mice expressing the transgene for human HLA A2/K^b (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with the synthetic peptides, as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 50µg of L726P peptide and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared. Cells were then resuspended at 7 x 10⁶ cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2 x 10⁻⁵ M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) L762P peptide- (5µg/ml) and 10mg/ml B₂-microglobulin- (3 µg/ml) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). After six days, cells (5 x 10⁵/ml) were restimulated with 2.5 x 10⁶/ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 5 x 10⁶/ml irradiated (3000 rads) A2/K^b-transgenic spleen feeder cells. Cells were cultured in the presence of 10U/ml IL-2. Cells were restimulated on a weekly basis as described, in preparation for cloning the line.

Peptide-specific cell lines were cloned by limiting dilution analysis with irradiated (20,000 rads) L762P peptide-pulsed EL4 A2Kb tumor cells (1 x 10⁴ cells/well) as stimulators and irradiated (3000 rads) A2/K^b-transgenic spleen cells as feeders (5 x 10⁵ cells/ well) grown in the presence of 10U/ml IL-2. On day 7, cells were restimulated as before. On day 14, clones that were growing were isolated and maintained in culture.

Cell lines specific for L762P-87 (SEQ ID NO: 226; corresponding to amino acids 87-95 of SEQ ID NO: 161), L726P-145 (SEQ ID NO: 227; corresponding to amino acids 145-153 of SEQ ID NO: 161), L726P-585 (SEQ ID NO: 228; corresponding to amino acids 585-593 of SEQ ID NO: 161), L762P-425 (SEQ ID NO: 229; corresponding to amino acids 425-433 of SEQ ID NO: 161), L762P(10)-424 (SEQ ID NO: 230; corresponding to amino acids 424-433 of SEQ ID NO: 161) and L762P(10)-458 (SEQ ID NO: 231; corresponding to amino acids 458-467 of SEQ ID

NO: 161) demonstrated significantly higher reactivity (as measured by percent specific lysis) against L762P peptide-pulsed EL4-A2/K^b tumor target cells than control peptide-pulsed EL4-A2/K^b tumor target cells.

5

EXAMPLE 7

IDENTIFICATION OF CD4 IMMUNOGENIC T CELL EPITOPES DERIVED
FROM THE LUNG CANCER ANTIGEN L762P

CD4 T cell lines specific for the antigen L762P (SEQ ID NO: 161) were
10 generated as follows.

A series of 28 overlapping peptides were synthesized that spanned approximately 50% of the L762P sequence. For priming, peptides were combined into pools of 4-5 peptides, pulsed at 20 micrograms/ml into dendritic cells for 24 hours. The dendritic cells were then washed and mixed with positively selected CD4⁺ T cells in 96
15 well U-bottomed plates. Forty cultures were generated for each peptide pool. Cultures were restimulated weekly with fresh dendritic cells loaded with peptide pools. Following a total of 3 stimulation cycles, cells were rested for an additional week and tested for specificity to antigen presenting cells (APC) pulsed with peptide pools using interferon-gamma ELISA and proliferation assays. For these assays, adherent
20 monocytes loaded with either the relevant peptide pool or an irrelevant peptide were used as APC. T cell lines that appeared to specifically recognize L762P peptide pools both by cytokine release and proliferation were identified for each pool. Emphasis was placed on identifying T cells with proliferative responses. T cell lines that demonstrated either both L762P-specific cytokine secretion and proliferation, or strong proliferation
25 alone were further expanded to be tested for recognition of individual peptides from the pools, as well as for recognition of recombinant L762P. The source of recombinant L762P was *E. coli*, and the material was partially purified and endotoxin positive. These studies employed 10 micrograms of individual peptides, 10 or 2 micrograms of an irrelevant peptide, and 2 or 0.5 micrograms of either L762P protein or an irrelevant,
30 equally impure, *E. coli* generated recombinant protein. Significant interferon-gamma production and CD4 T cell proliferation was induced by a number of L762P-derived

peptides in each pool. The amino acid sequences for these peptides are provided in SEQ ID NO: 232-251. These peptides correspond to amino acids 661-680, 676-696, 526-545, 874-893, 811-830, 871-891, 856-875, 826-845, 795-815, 736-755, 706-725, 706-725, 691-710, 601-620, 571-590, 556-575, 616-635, 646-665, 631-650, 541-560 and 586-605, respectively, of SEQ ID NO: 161.

CD4 T cell lines that demonstrated specificity for individual L762P-derived peptides were further expanded by stimulation with the relevant peptide at 10 micrograms/ml. Two weeks post-stimulation, T cell lines were tested using both proliferation and IFN-gamma ELISA assays for recognition of the specific peptide. A number of previously identified T cells continued to demonstrate L762P-peptide specific activity. Each of these lines was further expanded on the relevant peptide and, following two weeks of expansion, tested for specific recognition of the L762P-peptide in titration experiments, as well as for recognition of recombinant *E. coli*-derived L762P protein. For these experiments, autologous adherent monocytes were pulsed with either the relevant L762P-derived peptide, an irrelevant mammaglobin-derived peptide, recombinant *E. coli*-derived L762P (approx. 50% pure), or an irrelevant *E. coli*-derived protein. The majority of T cell lines were found to show low affinity for the relevant peptide, since specific proliferation and IFN-gamma ratios dramatically decreased as L762P peptide was diluted. However, four lines were identified that demonstrated significant activity even at 0.1 micrograms/ml peptide. Each of these lines (referred to as A/D5, D/F5, E/A7 and E/B6) also appeared to specifically proliferate in response to the *E. coli*-derived L762P protein preparation, but not in response to the irrelevant protein preparation. The amino acid sequences of the L762P-derived peptides recognized by these lines are provided in SEQ ID NO: 234, 249, 236 and 245, respectively. No protein specific IFN-gamma was detected for any of the lines. Lines A/D5, E/A7 and E/B6 were cloned on autologous adherent monocytes pulsed with the relevant peptide at 0.1 (A/D5 and E/A7) or 1 (D/F5) microgram/ml. Following growth, clones were tested for specificity for the relevant peptide. Numerous clones specific for the relevant peptide were identified for lines A/D5 and E/A7.

EXAMPLE 8

PROTEIN EXPRESSION OF LUNG TUMOR-SPECIFIC ANTIGENS

5 a) Expression of L514S in *E. coli*

The lung tumor antigen L514S (SEQ ID NO: 89) was subcloned into the expression vector pE32b at NcoI and NotI sites, and transformed into *E. coli* using standard techniques. The protein was expressed from residues 3-153 of SEQ ID NO: 89. The expressed amino acid sequence and the corresponding DNA sequence are
10 provided in SEQ ID NO: 252 and 253, respectively.

b) Expression of L762P

Amino acids 32-944 of the lung tumor antigen L762P (SEQ ID NO: 161), with a 6X His Tag, were subcloned into a modified pET28 expression vector,
15 using kanamycin resistance, and transformed into BL21 CodonPlus using standard techniques. Low to moderate levels of expression were observed. The determined DNA sequence of the L762P expression construct is provided in SEQ ID NO: 254.

From the foregoing it will be appreciated that, although specific
20 embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide, comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349 under moderately stringent conditions; and

(c) complements of sequences of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158,

160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349 or a complement of any of the foregoing polynucleotide sequences.

5

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 110, 112, 114, 152, 155, 156, 159, 161, 165, 166, 169, 170, 172, 174, 176, 226-252, 346, 348 and 350.

4. An isolated polynucleotide encoding at least 15 amino acid
10 residues of a lung tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29,
15 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349 or a
20 complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO:
25 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317,
30 323, 345, 347 and 349 or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349.
7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349 under moderately stringent conditions.
8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.
9. An expression vector, comprising a polynucleotide according to any one of claims claim 4-8.
10. A host cell transformed or transfected with an expression vector according to claim 9.
11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a lung tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84,

86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and
5 349_ or a complement of any of the foregoing polynucleotide sequences.

12. A fusion protein, comprising at least one polypeptide according to claim 1.

10 13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

14. A fusion protein according to claim 12, wherein the fusion
15 protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion protein comprises an affinity tag.

20

16. An isolated polynucleotide encoding a fusion protein according to claim 12.

17. A pharmaceutical composition, comprising a physiologically
25 acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- 30 (e) a polynucleotide according to claim 16.

18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

5 (a) sequences recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171,
10 173, 175, 177-224, 255-337, 345, 347 and 349 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii);
in combination with an immunostimulant.

15 26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

20

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient,
25 comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

30 (a) sequences recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and

349;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii) encoded by a polynucleotide recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349; and thereby inhibiting the development of a cancer in the patient.

30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29, wherein the cancer is lung cancer.

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349; and

(ii) complements of the foregoing polynucleotides; wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

33. A method according to claim 32, wherein the biological sample is blood or a fraction thereof.

34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.

5

35. A method for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) sequences recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349;

(ii) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 under moderately stringent conditions; and

(iii) complements of sequences of (i) or (ii);

(b) polynucleotides encoding a polypeptide of (a); and

(c) antigen presenting cells that express a polypeptide of (a);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

25

36. An isolated T cell population, comprising T cells prepared according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

30

38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient
5 with at least one component selected from the group consisting of:

(i) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

10 (1) sequences recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349;

(2) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158,
15 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);
(ii) polynucleotides encoding a polypeptide of (i); and
(iii) antigen presenting cells that expresses a polypeptide of
20 (i);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

25 39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) polypeptides comprising at least an immunogenic portion
30 of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence

selected from the group consisting of:

- (1) sequences recited in SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349;
- 5 (2) sequences that hybridize to a sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 under moderately stringent conditions; and
- (3) complements of sequences of (1) or (2);
- 10 (ii) polynucleotides encoding a polypeptide of (i); and
- (iii) antigen presenting cells that express a polypeptide of (i);
such that T cells proliferate;
- (b) cloning at least one proliferated cell to provide cloned T cells;
- and
- 15 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- 20 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 or a complement of any of the
- 25 foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

41. A method according to claim 40, wherein the binding agent is an

antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

5

43. A method according to claim 40, wherein the cancer is lung cancer.

44. A method for monitoring the progression of a cancer in a patient,
10 comprising the steps of:

(a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160,
15 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347 and 349 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained
20 from the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

25 45. A method according to claim 44, wherein the binding agent is an antibody.

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

30

47. A method according to claim 44, wherein the cancer is a lung

cancer.

48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

5 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347
10 and 349 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the
15 presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

20

50. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

25 51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a
30 polynucleotide sequence recited in any one of SEQ ID NO: 1-109, 111, 113, 115-151, 153, 154, 157, 158, 160, 162-164, 167, 168, 171, 173, 175, 177-224, 255-337, 345, 347

and 349 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained
5 from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

10 52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

53. A method according to claim 51, wherein the amount of
15 polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

54. A diagnostic kit, comprising:

(a) one or more antibodies according to claim 11; and
20 (b) a detection reagent comprising a reporter group.

55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.

25 56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

57. A kit according to claim 54, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent
30 groups, enzymes, biotin and dye particles.

58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349 or a complement of any of the foregoing polynucleotides.

59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 173, 175, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253, 254-258, 260, 262-264, 270, 272, 275, 276, 279-281, 286, 287, 291, 293, 295, 296, 300, 302, 308-310, 313, 315-317, 323, 345, 347 and 349.

20

60. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 59; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

25

SEQUENCE LISTING

<110> Corixa Corporation et al.

<120> COMPOUNDS AND METHODS FOR THERAPY
AND DIAGNOSIS OF LUNG CANCER

<130> 210121.45501PC

<140> PCT

<141> 2000-04-03

<160> 350

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 315

<212> DNA

<213> Homo sapien

<220>

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<223> n = A,T,C or G

<400> 1

gcagagacag actggtggtt gaacctggag gtgccaaaaa agccagctgc gggcccagga	60
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ttcatctcca gcagagacaa cggaggaggc tcccaccagg acggttctca ttatttatat	180
gttaatatgt ttgtaaactc atgtacagtt ttttttgggg gggaagcaat gggaanggta	240
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aaaaaaaaaaaa	315

<210> 2

<211> 380

<212> DNA

<213> Homo sapien

<400> 2

atttaggctt aagattttgt ttacccttgt tactaaggag caaattagta ttaaagtata	60
atatatataa acaaatacaa aaagttttga gtggttcagc ttttttatat tttttaatgg	120
cataactttt aacaacactg ctctgtaatg gggtgaactg tggactcag actgagataa	180
ctgaaatgag tggatgtata gtgttattgc ataattatcc cactatgaag caaagggact	240
ggataaattc ccagtctaga ttattagcct ttgttaacca tcaagcacct agaagaagaa	300
ttattggaat ttttgtcttc tgtaactggc actttggggg gtgacttata ttttgccttt	360
gtaaaaaaaaaaaa	380

<210> 3

<211> 346

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<220>
 <221> misc_feature
 <222> (1)...(346)
 <223> n = A,T,C or G

<400> 3
 ttgtaagtat acaatttttag aaaggattaa atgttattga tcatttttact gaatactgca 60
 catcctcacc atacaccatc cactttccaa taacattttaa tccttttctaa aattgtaagt 120
 atacaattgt actttctttg gattttcata acaaataac catagactgt taattttatt 180
 gaagtttctt taatggaatg agtcattttt gtcttggtgt tttgagggtta cctttgcttt 240
 gacttccaac aatttgatca tatagtgttg agctgtggaa atctttaagt ttattctata 300
 gcaataattt ctattnnnag annccngggn naaaannann annaaa 346

<210> 4
 <211> 372
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(372)
 <223> n = A,T,C or G

<400> 4
 actagtctca ttactccaga attatgctct tgtacctgtg tggctggggt tcttagtctg 60
 tggtttgggt tggttttttg aactgggtatg taggggtggt cacagttcta atgtaagcac 120
 tctcttctcc aagtgtgtgt ttgtggggac aatcattctt tgaacattag agaggaaggc 180
 agttcaagct gttgaaaaga ctattgctta tttttgtttt taaagacctt cttgacgtca 240
 tgtggacagt gcacgtgcct tacgctacat cttgttttct aggaagaagg ggatgcnggg 300
 aaggantggg tgctttgtga tggataaaac gnctaaataa cacaccttta cattttgaaa 360
 aaaacaaaac aa 372

<210> 5
 <211> 698
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(698)
 <223> n = A,T,C or G

<400> 5
 actagtanga tagaaacact gtgtcccag agtaaggaga gaagctacta ttgattagag 60
 cctaaccag gttaactgca agaagaggcg ggatactttc agctttccat gtaactgtat 120
 gcataaagcc aatgtagtcc agtttctaag atcatgttcc aagctaactg aatcccactt 180
 caatacacac tcatgaactc ctgatggaac aataacaggc ccaagcctgt ggtatgatgt 240
 gcacacttgc tagactcaga aaaaatacta ctctcataaa tgggtgggag tattttgggt 300
 gacaacctac tttgcttggc tgagtgaagg aatgatattc atatnttcat ttattccatg 360
 gacatttagt tagtgccttt tatataccag gcatgatgct gagtgacact cttgtgtata 420
 tntccaaatn ttngtncngt cgtgcacat atctgaaac ctatattaag antttcccaa 480
 natgangtcc ctggtttttc cagccactt gatcngtcaa ngatctcacc tctgntgtc 540
 ctaaaacctn ctntnnang gttagacngg acctctcttc tcccttcccg aanaatnaag 600
 tgtnggaaga nancncnch cccctctnch tncnncctng ccngctnnnc cncntgtngg 660

gggngccgcc cccgcggggg gaccccccn ttttcccc

698

<210> 6
 <211> 740
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(740)
 <223> n = A,T,C or G

<400> 6
 actagtcaaa aatgctaaaa taatttgga gaaaatattt ttttaagtagt gttatagttt 60
 catgtttatc ttttattatg tnttgtagag ttgtgtcttt tcactaatta cctatactat 120
 gccaatattt ccttatatct atccataaca tttatactac atttgtaaga gaatatgcac 180
 gtgaaactta acactttata aggtaaaaat gaggtttcca agatttaata atctgatcaa 240
 gttcttggtta tttccaaata gaatggactt ggtctgttaa ggggctaagg gagaagaaga 300
 agataagggt aaaagtgtt aatgaccaa cattctaaaa gaaatgcaaa aaaaaattta 360
 ttttcaagcc ttcgaactat ttaaggaaag caaatcatt tcctanatgc atatcatttg 420
 tgagantttc tcantaatat cctgaatcat tcatttcagc tnaggcttca tgttgactcg 480
 atatgtcatc tagggaaagt ctatttcagc gtccaaacct gttgcatag ttggttaggc 540
 tttccttta ntgtgaanta ttnacangaa attttctct tnanagttct tnatagggtt 600
 aggggtgtgg gaaaagcttc taacaatctg tagtggtncg tggtatctgt ncagaaccan 660
 aatnacgat cgnangaagg actgggtcta tttacangaa cgaatnatct ngtnnnnngt 720
 gttnncaact ccngggagcc 740

<210> 7
 <211> 670
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(670)
 <223> n = A,T,C or G

<400> 7
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 agcggccccg gctegatggc cccgtggtgc tcagttagca gcggcccgtc gcgctacgtg 120
 cttgggatgc aggagctgtt ccggggccac agcaagaccg cgagttcctg gcgcacagcg 180
 ccaaggtgca ctcggtggcc tggagttgcg acgggcgtcg cctacctcgg ggtcttcgac 240
 aagacgccac gtcttcttgc tgganaanga ccgttggtca aagaaaacaa ttatcgggga 300
 catggggata gtgtggacca ctttgttggc atccaagtaa tcctgacctt tttgttacgg 360
 cgtctggaga taaaaccatt cgcactctgg atgtgaggac taaaaaatgc attgccactg 420
 tgaacactaa aggggagaaac attaatatct gctggantcc tgatgggcan accattgctg 480
 tagcnacaag gatgatgtgg tgactttatt gatgccaaga aaccccgttc caaagcaaaa 540
 aaacanttcc aanttcgaag tcaccnaaat ctctggaac aatgaacatn aatatnttct 600
 tcctgacaat ggnccctggg tgtntcacat cctcagctnc cccaaaactg aancctgtnc 660
 natccacccc 670

<210> 8
 <211> 689
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(689)
 <223> n = A,T,C or G

<400> 8
 actagtatct aggaatgaac agtaaaagag gagcagttgg ctacttgatt acaacagagt 60
 aaatgaagta ctggatttgg gaaaacctgg ttttattaga acatatggaa tgaaagccta 120
 cacctagcat tgcctactta gccccctgaa ttaacagagc ccaattgaga caaaccctg 180
 gcaacaggaa attcaaggga gaaaaagtaa gcaacttggg ctaggatgag ctgactccct 240
 tagagcaaag ganagacagc cccattacc aaataccatt tttgcctggg gcttgtgcag 300
 ctggcagtg tccctgcccga gcatggcacc ttatngtttt gatagcaact tcgttgaatt 360
 ttcaccaact tattacttga aattataata tagcctgtcc gtttgcctgt tccaggctgt 420
 gatatatntt cctagtgggt tgacttttaa aataaataag gtttantttt cccccccnn 480
 cnntnctncc nntnctcnn cnntcccccc cnctcngtcc tccnnnttn gggggggccn 540
 ccccnccggn ggacccccct ttggtccctt agtggagggt natggcccct ggnnttatcc 600
 nggcctann tttcccctn nnaaatgntt cccctccca ntccnccac ctcaanccgg 660
 aagcctaagt ttntaccctg ggggtcccc 689

<210> 9
 <211> 674
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(674)
 <223> n = A,T,C or G

<400> 9
 gtccactctc ctttgagtgt actgtcttac tgtgcaactct gtttttcaac tttctagata 60
 taaaaaatgc ttgttctata gtggagtaag agctcacaca cccaaggcag caagataact 120
 gaaaaaagcg aggctttttt gccaccttgg taaaggccag ttcactgcta tagaactgct 180
 ataagcctga agggaagtag ctatgagact ttccattttt cttagttctc ccaataggct 240
 ccttcatgga aaaaggcttc ctgtaataat tttcacctaa tgaattagca gtgtgattat 300
 ttctgaaata agagacaaat tgggcccgcag agtcttcctg tgatttaaaa taaacaaccc 360
 aaagttttgt ttggtcttca ccaaaggaca tactctaggg ggtatgttgt tgaagacatt 420
 caaaaacatt agctgttctg tctttcaatt tcaagttatt ttggagactg cctccatgtg 480
 agttaattac tttgctctgg aactagcatt attgtcatta tcatcacatt ctgtcatcat 540
 catctgaata atattgtgga tttccccctc tgcttgcatc ttcttttgac tcctctggga 600
 anaaatgtca aaaaaaaagg tcgatctact cngcaaggnc catctaata ctgcgctgga 660
 aggaccnct gcc 674

<210> 10
 <211> 346
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(346)
 <223> n = A,T,C or G

<400> 10

actagtctgc	tgatagaaag	cactatacat	cctattgttt	ctttctttcc	aaaatcagcc	60
ttctgtctgt	aacaaaaatg	tactttatag	agatggagga	aaaggtctaa	tactacatag	120
ccttaagtgt	ttctgtcatt	gttcaagtgt	attttctgta	acagaaacat	atttggaatg	180
tttttctttt	ccccttataa	attgtaattc	ctgaaatact	gctgctttaa	aaagtcaccac	240
tgtcagatta	tattatctaa	caattgaata	ttgtaaatat	acttgtctta	cctctcaata	300
aaagggtact	tttctattan	nnagnngnnn	gnnnnataaa	anaaaa		346

<210> 11
<211> 602
<212> DNA
<213> Homo sapien

<400> 11						
actagtaaaa	agcagcattg	ccaaataatc	cctaattttc	cactaaaaat	ataatgaaat	60
gatgttaagc	tttttgaaaa	gttttaggta	aacctactgt	tgtagatta	atgtatttgt	120
tgcttccctt	tatctggaat	gtggcattag	cttttttatt	ttaacctctt	ttaattotta	180
ttcaattcca	tgacttaagg	ttggagagct	aaacactggg	atttttggat	aacagactga	240
cagttttgca	tattataat	cggcattgta	catagaaagg	atatggctac	cttttgtaa	300
atctgcactt	tcataatc	aaaaaaggga	aatgaagtta	taaatcaatt	tttgtataat	360
ctgtttgaaa	catgagtttt	atttgcttaa	tattagggct	ttgccccttt	tctgtaagtc	420
tcttgggata	ctgtgtagaa	ctgttctcat	taaacaccaa	acagttaagt	ccattctctg	480
gtactagcta	caaattcggt	ttcatattct	acttaacaat	ttaaataaac	tgaaatattt	540
ctagatgggc	tacttctgtt	catataaaaa	caaaacttga	tttccaaaaa	aaaaaaaaaa	600
aa						602

<210> 12
<211> 685
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (685)
<223> n = A,T,C or G

<400> 12						
actagtccctg	tgaaagtaca	actgaaggca	gaaagtgtta	ggatttttgc	tctaatgttc	60
attatcatgg	tattgatgga	cctaagaaaa	taaaaattag	actaagcccc	caaataagct	120
gcatgcattt	gtaacatgat	tagtagattt	gaatatatag	atgtagtatn	ttgggtatct	180
aggtgtttta	tcattatgta	aaggaattaa	agtaaaggac	tttgtagttg	tttttattaa	240
atatgcatat	agtagagtgc	aaaaatatag	caaaaatana	aactaaaggt	agaaaagcat	300
tttagatatg	ccttaatnta	nnaactgtgc	caggtggccc	tcggaataga	tgccaggcag	360
agaccagtgc	ctgggtgggtg	cctccccttg	tctgcccccc	tgaagaactt	ccctcacgtg	420
angtagtgcc	ctcgtagggtg	tcacgtggan	tantggganc	aggccgnncn	gtnanaagaa	480
ancanngtga	nagtttcncc	gtngangcng	aactgtccct	gngccnnnac	gctcccanaa	540
cntntccaat	ngacaatcga	gtttccnnnc	tcnngnaacc	tngccgnnnn	cnngcccnnc	600
cantntgnta	accccgcgcc	cggatcgctc	tcnnntcggt	ctcncncnaa	ngggntttcn	660
cnnccgccgt	cncnnccccg	cnncc				685

<210> 13
<211> 694
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
 <222> (1) ... (694)
 <223> n = A,T,C or G

<400> 13
 cactagtcac tcattagcgt tttcaatagg gctcttaagt ccagtagatt acgggtagtc 60
 agttgacgaa gatctggttt acaagaacta attaaatggt tcattgcatt tttgtaagaa 120
 cagaataatt ttataaaatg tttgtagttt ataattgccg aaaataattt aaagacactt 180
 tttctctgtg tgtgcaaagtg tgtgtttgtg atccattttt tttttttttt taggacacct 240
 gtttactagc tagctttaca atatgccaaa aaaggatttc tccctgaccc catccgtggg 300
 tcaccctctt tcccccccat gctttttgcc ctagtattata acaaaggaat gatgatgatt 360
 taaaaagtag ttctgtatct tcagtatctt ggtcttccag aaccctctgg ttgggaaggg 420
 gatcattttt tactgggtcat ttcccttttg agtgactac tttaacagat ggaaagaact 480
 cattggccat ggaaacagcc gangtggttg gagccagcag tgcattggcac cgtccggcat 540
 ctggcgtgat tgggtctggct gccgtcattg tcagcacagt gccatgggac atggggaana 600
 ctgactgcac ngccaatggg tttcatgaag aatacngcat ncnngtgat cactgnancc 660
 angacgctat gggggncana gggccanttg ctte 694

<210> 14
 <211> 679
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (679)
 <223> n = A,T,C or G

<400> 14
 cagccgctg catctgtatc cagcgccang tcccgccagt cccagctgcg cgcgccccc 60
 agtcccgnac cggttcggcc cangctnagt tagncctcac catnccggtc aaaggangca 120
 ccaagtgcac caaatacctg cngtncggat ntaaattcat cttctggctt gccgggattg 180
 ctgtcctgc cattggacta nggtccgat ncgactctca gaccanganc atcttcganc 240
 naganactaa tnatnattnt tccagcttct acacaggagt ctatattctg atcggtaccg 300
 gcncctctnt gatgctgggt ggcttctga gctgctgcgg ggctgtgcaa gagtcccant 360
 gcatgctggg actgttcttc ggcttctct tggatgatn cgccattgaa atacctgcgg 420
 ccatctgggg atattccact ncgatnatgt gattaaggaa ntccacggag ttttacaagg 480
 acacgtacaa cnacctgaaa accnnggatg anccccaccg ggaancnctg aangccatcc 540
 actatgcgtt gaactgcaat ggtttggctg gggnccttga acaatttaat cncatacatc 600
 tgccccann aaaggacntn ctcgannctt tcnccgtgna attcngttct gatnccatca 660
 cagaagtctc gaacaatcc 679

<210> 15
 <211> 695
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (695)
 <223> n = A,T,C or G

<400> 15
 actagtggat aaaggccagg gatgctgctc aacctcctac catgtacagg gacgtctccc 60
 cattacaact acccaatccg aagtgtcaac tgtgtcagga ctaanaaacc ctgggttttga 120

```

ttaaaaaagg gcctgaaaaa aggggagcca caaatctgtc tgcttcctca cnttantcnt 180
tggcaaatna gcattctgtc tcnttggtc cngcctcanc ncaaaaaanc ngaactcnat 240
cnggccagc aatacatctc ncaatnaacn aaattganca aggcnnntggg aaatgccnga 300
tgggattatc ntccgcttgt tgancctcta agtttcttcc ccttcattcn accctgccag 360
ccnagtctctg ttagaaaaat gccngaattc naacnccggg tttctactc ngaatttaga 420
tctncanaaa ctctcctggcc acnattcnaa ttnanggnca cgnacanatn ccttccatna 480
ancncacccc acntttgana gccangacaa tgactgcntn aantgaaggc ntgaaggaan 540
aactttgaaa ggaaaaaaa ctttggttcc ggccccctcc aacncttctg tgttnancac 600
tgccttctng naaccctgga agcccnngga cagtgttaca tgttgttcta nnaaacngac 660
ncttnaatnt cnatcttccc nanaacgatt ncnc 695

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<210> 16
<211> 669
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(669)
<223> n = A,T,C or G

```

```

<400> 16
cgccgaagca gcagcgagc ttgtccccgt tccccctccc ccttccttcc tccgggttgc 60
ttccccggcc ccttacactc cacagtcccg gtccccgcat gtcccagaaa caagaagaag 120
agaaccctgc ggaggagacc ggcgaggaga agcaggacac gcaggagaaa gaaggatttc 180
tgcctgagag agctgaagag gcaaagctaa aggccaaata cccaagccta ggacaaaagc 240
ctggaggctc cgacttcttc atgaagagac tccagaaagg gcaaaagtac tttgactcng 300
gagactacaa catggccaaa gccaacatga agaataagca gctgccaagt gcangaccag 360
acaagaacct ggtgactggt gatcacatcc ccaccccaca ggatctgccc agagaaaagtc 420
ctcgctcgtc accagcaagc ttgcggttgg ccaagttgaa tgatgctgcc ggggctctgc 480
canatctgag acgcttccct ccctgcccc cccgggtcct gtgctggctc ctgcccttcc 540
tgcttttgca gccangggtc aggaagtggc ncnggtngtg gctggaaagc aaaacccttt 600
cctgttggtg tcccacccat ggagcccctg gggcgagccc angaacttga ncctttttgt 660
tntcttncc 669

```

```

<210> 17
<211> 697
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(697)
<223> n = A,T,C or G

```

```

<400> 17
gcaagatatg gacaactaag tgagaaggta atnctctact gctctagntn ctccnggcnn 60
gacgcgtga ggagannnac gctggcccan ctgccggcca cacacgggga tcntggtnat 120
gcctgcccac gggancccca ncnetcgan cccatntcac acccgnnccn tncgcccacn 180
neetggctcn cncngeccng nccagctcnc gnccectccc gccnnnetcn ttnnctctc 240
cncnccctcc ncnacnacct cctaccncg gctccctccc cagccccccc ccgcaanect 300
ccacnacncc ntcnncncca ancncnctc gcnctengcc cngccccct gccccccgcc 360
cncnacnncg cgnctccccg cgcncgcngc ctnccectcc cccacnacag ncncacccgc 420
agnacgcnc tccgcccnc gacgcccnn cccgcgcgc tcacctcat ggnccnacng 480
ccccgctcnc nccnetgcnc gccgncnngg cgccecgccc cnnccngntn ccncncngng 540

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ccccngcngn angcngtgcg cnnccangncc gngccggnnn ncaccctccg nccnccgccc 600
cgcccgtctg gggtccccgc cncgcggntc antccccncc cntnccgccca ctntccgntc 660
cnnnctcnc gctcngcgcn cgcccnccnc cccccc 697

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<210> 18
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

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<400> 18
ctcgtgtgaa ggggtgcagta cctaagccgg agcggggtag aggcggggccg gcaccccctt 60
ctgacctcca gtgcccgcgg cctcaagatc agacatggcc cagaacttga acgacttggc 120
gggacggctg cccgcccggc cccggggcat gggcacggcc ctgaagctgt tgctgggggc 180
cggcgcgctg gcctacggtg tgcgcgaatc tgtgttcacc gtggaaggcg ggcncagagc 240
catcttcttc aatcggatcg gtggagtgc caggacacta tcctggggccg anggccttca 300
cttcaggatc cttggttcca gtaccccanc atctatgaca ttcggggccag acctcgaaaa 360
aatctcctcc ctacaggctc caaagacctc cagatgggtga atatctccct gcgagtgttg 420
tctcgaccaa tgctcangaa cttcctaaca tgttccancg cctaagggtc ggactacnaa 480
gaacgantgt tgccgtccat tgtcacgaag tgctcaagaa tttnggtggc caagttcaat 540
gncctcacnn ctgatcnccc agcggggcca agttanccct ggttgatccc cgggganctg 600
acnnaaaagg gccaaaggact tcccctcatc ctggataatg tggccntcac aaagctcaac 660
tttanccacc 670

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<210> 19
<211> 606
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G

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<400> 19
actagtgcc aacctagctc ccaggccagt tctctgaatg tcgaggagtt ccaggatctc 60
tggcctcagt tgtccttggt tattgatggg ggacaaattg gggatggcca gagccccgag 120
tgtgccttg gctcaactgt ggttgatttg tctgtgcccg gaaagtgttg catcattcgt 180
ccaggctgtg ccctggaaag tactacagcc atcctccaac agaagtacgg actgctcccc 240
tcacatgcgt cctacctgtg aaactctggg aagcaggaag gcccaagacc tgggtgtgga 300
tactatgtgt ctgtccactg acgactgtca aggcctcatt tgcagaggcc accggagcta 360
gggcactagc ctgactttta aggcagtgtg tctttctgag cactgtagac caagcccttg 420
gagctgctgg tttagccttg cacctgggga aaggatgtat ttatttgtat tttcatatat 480
cagccaaaag ctgaatggaa aagttnagaa cattcctagg tggccttatt ctaataagtt 540
tcttctgtct gttttgtttt tcaattgaaa agttattaaa taacagattt agaattagtt 600
gagacc 606

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<210> 20
<211> 449
<212> DNA
<213> Homo sapien

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<400> 20

actagtaa	aacagcag	ca gaaacat	cag tatcag	cagc gtcgcc	agca ggagaat	atg	60
cagcgcca	gagcggag	aga accccc	gctc cctgag	gagg acctgt	ccaa actctt	caaa	120
ccaccaca	gcgcctgc	cag gatgg	actcg ctgctc	attg caggcc	agat aaacac	ttac	180
tgccaga	aaca tcaagg	agt cactgc	ccaa aactta	ggca agctct	tcac ggccc	aggct	240
cttcaag	aat acaaca	cta agaaa	aggaa gtttcc	agaa aaga	agttaa	catga	300
ctcat	ccaggg	caac tcttg	gaaga aatat	atttg catatt	gaaa agcac	agag	360
atctctt	tag tgcatt	gcc gatttt	ggct ataac	agtg tttct	agcc ataata	aaaat	420
aaaacaaa	at cttgact	gct tgctca	aaaa				449

<210> 21

<211> 409

<212> DNA

<213> Homo sapien

<400> 21

tatcaat	caa ctggt	gaata attaa	acaat gtgtg	gtgtg atcata	caaa gggtac	cact	60
caatgata	aaa aggaac	aagc tgcct	tatatg tggaac	aaca tggat	gcatt tcagaa	actt	120
tatgttg	agt gaaaga	acaa acacg	gagaa catact	atgtt	ctcttt atgtac	catt	180
acagaaa	ataa aaacag	agggc aaccac	cttt gaggc	agtat ggagt	gagat agact	ggaaa	240
aaggaag	gaa ggaact	cta cgctg	atgga aatgt	ctgtg tcttc	attgg gtggt	tagtta	300
tggtggg	gata tacatt	tgtc aaaatt	tattt gaact	atata ctaa	agaact ctgcatt	ttta	360
ttgggat	gta aataat	acct caatt	aaaaa gacaaaa	aaaaa			409

<210> 22

<211> 649

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(649)

<223> n = A,T,C or G

<400> 22

acaatttt	cca ttatct	taag cacatt	gtac atttct	acag aacct	gtgat tattct	cgca	60
tgataagg	gat ggtact	tgca tatggt	gaat tactact	gtt gacagt	ttcc gcagaa	atcc	120
tatttcag	tg gacca	acatt gtggc	atggc agcaa	atgcc aacatt	tttgtt ggaat	agcag	180
caaatcta	ca agagac	cctg gttgg	ttttt cgtttt	gtttt tcttt	gtttt ttcccc	cttc	240
tcctgaat	ca gcagg	gatgg aang	agggta ggga	agttat gaatt	actcc ttccag	tagt	300
agctctga	ag tgcaca	ttt aatat	cagtt ttttt	taaac atgatt	ctag ttnaat	gtag	360
aagagaga	ag aaagag	gaag tgttc	acttt tttata	acac tgatt	tagaa atttg	atg	420
ttatatc	agt agttc	tggagg tatt	gatagc ttgct	ttatt tctgc	cttta cgttg	acagt	480
gttgaag	cag ggtga	ataac taggg	gcata tatatt	ttttt ttttt	gtaa gctgtt	tcac	540
gatgtttt	ct ttgga	atttc cggata	agtt caggaa	aaaca tctgc	atgtt gttat	ctagt	600
ctgaagtt	cn tatcca	ctc attaca	acaa aaacn	cccag aacgg	nttg		649

<210> 23

<211> 669

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(669)

<223> n = A,T,C or G

<400> 23

actagtgccg	tactggctga	aatccctgca	ggaccaggaa	gagaaccagt	tcagactttg	60
tactctcagt	caccagctct	ggaattagat	aaattccttg	aagatgtcag	gaatgggac	120
tatcctctga	cagcctttgg	gctgcctcgg	ccccagcagc	cacagcagga	ggaggtgaca	180
tcacctgtcg	tgccccctc	tgtcaagact	ccgacacctg	aaccagctga	ggtggagact	240
cgcaagggtg	tgctgatgca	gtgcaacatt	gagtcggtgg	aggagggagt	caaacaccac	300
ctgacacttc	tgctgaagtt	ggaggacaaa	ctgaaccggc	acctgagctg	tgacctgatg	360
ccaaatgaga	atatccccga	gttggcggct	gagctggtgc	agctgggctt	cattagttag	420
gctgaccaga	gccggttgac	ttctctgcta	gaagagactt	gaacaagttc	aattttgcca	480
ggaacagtac	cctcaactca	gccgctgtca	ccgtctcttc	ttagagctca	ctcgggccag	540
gccctgatct	gcgtgtggc	tgtcctggac	gtgctgcacc	ctctgtcctt	ccccccagtc	600
agtattacct	gtgaagccct	tcctctcttt	attattcagg	anggctgggg	gggctccttg	660
nttctaacc						669

<210> 24

<211> 442

<212> DNA

<213> Homo sapien

<400> 24

actagtacca	tcttgacaga	ggatacatgc	tcccaaaacg	tttgttacca	cacttaaaaa	60
tcactgccat	cattaagcat	cagtttcaaa	attatagcca	ttcatgattt	actttttcca	120
gatgactatc	attattctag	tcctttgaat	ttgtaagggg	aaaaaaaaa	aaaacaaaaa	180
cttacgatgc	acttttctcc	agcacatcag	atttcaaatt	gaaaattaaa	gacatgctat	240
ggtaatgcac	ttgctagtac	tacacacttt	ggtacaacaa	aaaacagagg	caagaaacaa	300
cggaaagaga	aaagccttcc	tttgttgccc	cttaaactga	gtcaagatct	gaaatgtaga	360
gatgatctct	gacgatacct	gtatgttctt	attgtgtaaa	taaaattgct	ggtatgaaat	420
gacctaaaaa	aaaaaaaaa	aa				442

<210> 25

<211> 656

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(656)

<223> n = A,T,C or G

<400> 25

tgcaagtacc	acacactgtt	tgaattttgc	acaaaaagtg	actgtaggat	caggtgatag	60
ccccggaatg	tacagtgtct	tggtgcacca	agatgccttc	taaaggctga	cataccttgg	120
accctaattg	ggcagagagt	atagccctag	cccagtgggtg	acatgaccac	tccttttggg	180
aggcctgagg	tagaggggag	tggtatgtgt	tttctcagtg	gaagcagcac	atgagtgggt	240
gacaggatgt	tagataaagg	ctctagttag	ggtgtcattg	tcatttgaga	gactgacaca	300
ctcctagcag	ctggtaaagg	ggtgctggan	gccatggagg	anctctagaa	acattagcat	360
gggctgatct	gattacttcc	tggcatcccc	ctcactttta	tgggaagtct	tattagangg	420
atgggacagt	tttccatata	cttgctgtgg	agctctggaa	cactctctaa	atttccctct	480
attaaaaatc	actgccctaa	ctacacttcc	tccttggaag	aatagaaatg	gaactttctc	540
tgacatantt	cttggcatgg	ggagccagcc	acaaatgana	atctgaacgt	gtccaggttt	600
ctcctganac	tcactacat	agaattgggt	aaacctctcc	ttggaataag	gaaaaa	656

<210> 26
 <211> 434
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (434)
 <223> n = A,T,C or G

<400> 26
 actagttcag actgccacgc caaccccaga aaatacccca catgccagaa aagtgaagtc 60
 ctaggtgttt ccatctatgt ttcaatctgt ccatctacca ggcctcgcga taaaaacaaa 120
 acaaaaaaac gctgccaggt tttagaagca gttctggtct caaaaccatc aggatcctgc 180
 caccagggtt cttttgaaat agtaccacat gtaaaaggga atttggcttt cacttcatct 240
 aataactgaa ttgtcaggct ttgattgata attgtagaaa taagtagcct tctgttgagg 300
 gaataagtta taatcagtat tcatctcttt gttttttgtc actcttttct ctctaattgt 360
 gtcatttgta ctgtttgaaa aatatttctt ctatnaaatt aaactaacct gccttaaaaa 420
 aaaaaaaaaa aaaa 434

<210> 27
 <211> 654
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (654)
 <223> n = A,T,C or G

<400> 27
 actagtccaa cacagtcaga aacattgttt tgaatcctct gtaaaccaag gcattaatct 60
 taataaacca ggatccattt aggtaccact tgatataaaa aggatatcca taatgaatat 120
 tttatactgc atcctttaca ttagccacta aatacgttat tgcttgatga agacctttca 180
 cagaatccta tggattgcag catttcactt ggctacttca taccatgcc ttaaagaggg 240
 gcagttttctc aaaagcagaa acatgccgcc agttctcaag ttttcctcct aactccattt 300
 gaatgtaagg gcagctggcc cccaatgtgg ggaggtccga acattttctg aattccattt 360
 ttcttgttcg cggctaaatg acagtttctg tcattactta gattccgac tttcccaaag 420
 gtgttgattt acaaagaggg cagctaatac cagaaatcat gaccctgaaa gagagatgaa 480
 attcaagctg tgagccaggc agganctcag tatggcaaag gtcttgagaa tcngccattt 540
 ggtacaaaaa aaatttttaa gcntttatgt tataccatgg aaccatagaa anggcaaggg 600
 aattgttaag aanaatttta agtgtccaga ccanaanga aaaaaaaaaa aaaa 654

<210> 28
 <211> 670
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (670)
 <223> n = A,T,C or G

<400> 28
 cgtgtgcaca tactgggagg atttccacag ctgcacggtc acagccctta cggattgcc 60

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ggaaggggcg aaagatatgt gggataaact gagaaaagaa nccaaaaaacc tcaacatcca 120
aggcagctta ttcgaactct gcggcagcgg caacggggcg gcgggggtccc tgctcccggc 180
gttcccgggtg ctccctgggtg ctctctcggc agcttttagcg acctgncttt ccttctgagc 240
gtggggccag ctccccccgc ggcgcccacc cacnctcact ccattgctccc ggaaatcgag 300
aggaagatca ttagttcttt ggggacgttn gtgattctct gtgatgctga aaaacactca 360
tatagggaat gtgggaaatc ctganccttt tnttatntcg tntgatttct tgtgttttat 420
ttgccaaaat gttaccaatc agtgaccaac cnagcacagc caaaaatcgg acntcngctt 480
tagtccgtct tcacacacag aataagaaaa cggcaaaccc accccacttt tnantttnat 540
tattactaan ttttttctgt tgggcaaaaag aatctcagga acngccctgg ggccnccgta 600
ctanagttaa ccnagctagt tncatgaaaa atgatgggct ccnctcaat gggaaagcca 660
agaaaaagnc 670

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<210> 29
<211> 551
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(551)
<223> n = A,T,C or G

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<400> 29
actagtcctc cacagcctgt gaatccccct agacctttca agcatagtga gcggagaaga 60
agatctcagc gtttagccac cttacccatg cctgatgatt ctgtagaaaa ggtttcttct 120
ccctctccag ccaactgatg gaaagtattc tccatcagtt ctcaaaatca gcaagaatct 180
tcagtaccag aggtgcctga tgttgacacat ttgccacttg agaagctggg accctgtctc 240
cctcttgact taagtctgtg ttcagaagtt acagcaccgg tagcctcaga ttctctttac 300
cgtaatgaat gtcccagggc agaaaaagag gatacncaga tgcttccaaa tcttcttccc 360
aaagcaatag ctgatgggaa gaggagctcc agcagcagca ggaatatcga aaacagaaaa 420
aaaagtgaat ttgggaagac aaaagctcaa cagcatttgg taaggagaaa aganaagatg 480
aggaaggaag agagaagaga gacnaagatc nctacggacc gnnncggaag aagaagaagn 540
aaaaaanaaa a 551

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<210> 30
<211> 684
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(684)
<223> n = A,T,C or G

```

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<400> 30
actagttcta tctggaaaaa gcccgggttg gaagaagctg tggagagtgc gtgtgcaatg 60
cgagactcat ttcttggaag catccctggc aaaaatgcag ctgagtacaa ggttatcact 120
gtgatagaac ctggactgct ttttgagata atagagatgc tgcagtctga agagacttcc 180
agcacctctc agttgaatga attaatgatg gcttctgagt caactttact ggctcaggaa 240
ccacgagaga tgactgcaga tgtaatcgag cttaaaggga aattcctcat caacttagaa 300
ggtggtgata ttcgtgaaga gtcttcctat aaagtaattg tcatgccgac tacgaaagaa 360
aatgcccc gttgttgga gtatacagcg ggagtcttca gatacactgt gtcctcgatg 420
tgcagaagtt gtcagtggga aaatagtatt aacagctcac tcgagcaaga accctcctga 480
cagtactggg ctagaagttt ggatggatta tttacaatat aggaaagaaa gccaagaatt 540
aggtnatgag tggatgagta aatggtggan gatggggaat tcaaatcaga attatggaag 600

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aagttnttcc tgttactata gaaaggaatt atgtttatatt acatgcagaa aatatanatg 660
 tgtggtgtgt accgtggatg gaan 684

<210> 31
 <211> 654
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (654)
 <223> n = A,T,C or G

<400> 31
 ggcagaaaaa ggaaccaata tttcagaaac aagcttaata ggaacagctg cctgtacatc 60
 aacatcttct cagaatgacc cagaagttat catcgtggga gctggcgtgc ttggctctgc 120
 tttggcagct gtgctttcca gagatggaag aaagggtgaca gtcattgaga gagacttaaa 180
 agagcctgac agaatagttg gagaattcct gcagccgggt gggtatcatg ttctcaaaga 240
 ccttggtctt ggagatacag tggaagggtc tgatgccag gttgtaaatg gttacatgat 300
 tcatgatcag ggaaagcaaa tcagangttc agattcctta ccctctgtca gaaaacaatc 360
 aagtgcagag tggaagagct ttccatcacg gaagattcat catgagtctc cggaaagcag 420
 ctatggcaga gcccaatgca aagtttattg aagggtgttg gttacagtta ttagaggaag 480
 atgatgttgat gatgggagtt cagtacaagg ataaagagac tgggagatat caaggaactc 540
 catgctccac tgactgttgat tgcagatggg cttttctcca anttcaggaa aagcctggtc 600
 tcaataaagt ttctgtatca ctcatgttggt tggcttctta tgaagaatgc nccc 654

<210> 32
 <211> 673
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (673)
 <223> n = A,T,C or G

<400> 32
 actagtgaag aaaaagaaat tctgatacgg gacaaaaatg ctcttcaaaa catcattctt 60
 tatcacctga caccaggagt tttcattgga aaaggatttg aacctgggtg tactaacatt 120
 ttaaagacca cacaaggaag caaaatcttt ctgaaagaag taaatgatac acttctggtg 180
 aatgaattga aatcaaaaaga atctgacatc atgacaacaa atgggtgtaat tcatgttgta 240
 gataaaactcc tctatccagc agacacacct gttggaaatg atcaactgct ggaaataact 300
 aataaattaa tcaaatacat ccaaattaag tttgttcgtg gtagcacctt caaagaaatc 360
 cccgtgactg tctatnagcc aattattaaa aaatacacca aaatcattga tgggagtgcc 420
 tgtgggaaat aactgaaaaa gagaccgaga agaacgaatc attacagggtc ctgaaataaa 480
 atacctagga tttctactgg aggtggagaa acagaagaac tctgaagaaa ttgttacaag 540
 aagangtccc aaggtcacca aattcattga aggtgggtgat ggtctttatt tgaagatgaa 600
 gaaattaaaa gacgcttcag ggagacnccc catgaaggaa ttgccagcca caaaaaaatt 660
 cagggattag aaa 673

<210> 33
 <211> 673
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (673)
 <223> n = A,T,C or G

<400> 33
 actagttatt tactttcctc cgcttcagaa ggtttttcag actgagagcc taagcatact 60
 ggatctgttg tttcttttgg gtctcacctc atcagtgtgc atagtggcag aaattataaa 120
 gaaggttgaa aggagcaggg aaaagatcca gaagcatggt agttcgacat catcatcttt 180
 tcttgaagta tgatgcatat tgcattatct tatttgcaaa ctaggaattg cagtctgagg 240
 atcatttaga agggcaagtt caagaggata tgaagatttg agaacttttt aactattcat 300
 tgactaaaaa tgaacattaa tgttnaagac ttaagacttt aacctgctgg cagtcccaaa 360
 tgaaattatg caactttgat atcatattcc ttgatttaaa ttgggctttt gtgattgant 420
 gaaactttat aaagcatatg gtcagttatt tnattaaaaa ggcaaaacct gaaccacctt 480
 ctgcacttaa agaagtctaa cagtacaaat acctatctat cttagatgga tntatttntt 540
 tntattttta aatattgtac tatttatggg nggtggggct ttcttactaa tacacaaatn 600
 aatttatcat ttcaanggca ttctatttgg gtttagaagt tgattccaag nantgcatat 660
 ttegtactg tnt 673

<210> 34
 <211> 684
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (684)
 <223> n = A,T,C or G

<400> 34
 actagtttat tcaagaaaag aacttactga ttctctgtgt cctaaagcaa gagtggcagg 60
 tgatcagggc tgggtgtagca tccggttcct ttagtgagc taactgcatt tgtcactgat 120
 gaccaaggag gaaatcacta agacatttga gaagcagtg tatgaacgtt cttggacaag 180
 ccacagttct gagccttaac cctgtagttt gcacacaaga acgagctcca cctcccttc 240
 ttcaggagga atctgtgcgg atagattggc tggacttttc aatggttctg ggttgcaagt 300
 gggcactgtt atggctgggt atggagcgga cagccccagg aatcagagcc tcagcccggc 360
 tgcttggttg gaaggtacag gtgttcagca ccttcggaaa aagggcataa agtngtgggg 420
 gacaattctc agtccaagaa gaatgcattg accattgctg gctatttgct tncctagtat 480
 gaattggatn catttttgac cangatnntt ctncatgct ttnttgcaat gaaatcaaat 540
 cccgcattat ctacaagtgg tatgaagtc tgcncccc agagaggctg ttcaggcnat 600
 gtcttccaag ggcagggtgg gttacaccat ttacctccc ctctcccc agattatgna 660
 cncagaagga atttntttcc tccc 684

<210> 35
 <211> 614
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (614)
 <223> n = A,T,C or G

<400> 35
 actagtccaa cgcgttngcn aatattcccc tggtagccta ctctcttacc cccgaatatt 60

ggtaagatcg	agcaatggct	tcaggacatg	ggttctcttc	tcctgtgatc	attcaagtgc	120
tcactgcatg	aagactggct	tgtctcagtg	tntcaacctc	accagggctg	tctcttggtc	180
cacacctcgc	tcctgttag	tgccgtatga	cagcccccat	canatgacct	tggccaagtc	240
acggtttctc	tgtggtcaat	gttggtnggc	tgattgggtg	aaagtanggt	ggaccaaagg	300
aagncncgtg	agcagncanc	nccagttctg	caccagcagc	gcctccgtcc	tactnggggtg	360
ttcncgtttc	tcctggccct	gngtgggcta	nggcctgatt	cgggaaanag	cctttgcang	420
gaaggganga	taantgggat	ctaccaattg	attctggcaa	aacnatntct	aagattnttn	480
tgctttatgt	ggganacana	tctanctctc	atttnttget	gnanatnaca	ccctactcgt	540
gntcgancnc	gtcttcgatt	ttcgganaca	cnccantnaa	tactggcggt	ctgttggttaa	600
aaaaaaaaaa	aaaa					614

<210> 36
 <211> 686
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(686)
 <223> n = A,T,C or G

<400> 36						
gtggctggcc	cggttctccg	cttctcccca	tccctactt	tcctccctcc	ctccctttcc	60
ctccctcgtc	gactgttget	tgctggctgc	agactccctg	accctccct	caccctcccc	120
taacctcggg	gccaccgat	tgcccttctt	tcctgtttgc	ccagcccagc	cctagtgtca	180
gggcgggggc	ctggagcagc	ccgaggcact	gcagcagaag	ananaaaaga	cacgacnaac	240
ctcagctcgc	cagtcgggtc	gctngcttcc	cgccgcgatg	caatnagaca	gacgccgtcc	300
acctgctctg	ggcacacgcg	accctgtggt	gatttggcct	tcagtggcat	cacccttatg	360
ggtatttctt	aatcagcgct	tgcaaagatg	gttaacctat	gctacgccag	ggagatacac	420
gagactggat	tggaacattt	ttggggctta	aaggtctggt	tggggtgcaa	cactgaataa	480
ggatggcacc	aaagcagcta	cagcagctgc	agatttcaca	gcccagtggt	gggatgctgt	540
ctcagganat	naattgataa	cctggtcat	aacacattgt	caagaatgtg	gatttcccca	600
ggatattatt	atttgtttac	cggggganag	gataactggt	tcnctatttt	taattgaaca	660
aactnaaaca	aanctaagg	aatcc				686

<210> 37
 <211> 681
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(681)
 <223> n = A,T,C or G

<400> 37						
gagacanacn	naacgtcang	agaanaaaag	angcatggaa	cacaanccag	gcncgatggc	60
caccttccca	ccagcancca	gcgcccccca	gcngccccca	ngnccggang	accangactc	120
cancctgnat	caatctganc	tctattcctg	gcccattncct	acctcggagg	tggangccgn	180
aaaggtcgca	cnnncagaga	agctgctgcc	ancaccancc	gccccnnccc	tgncgggctn	240
nataggaaac	tggtgaccnn	gctgcanaat	tcatacagga	gcacgcgang	ggcacnnnct	300
cacactgagt	tnnngatgan	gcctnaccan	ggacctnccc	cagcnnattg	annaacnggac	360
tgccggaggaa	ggaagacccc	gnacnggatc	ctggccggcn	tgccaccccc	ccacccctag	420
gattatnccc	cttgactgag	tctctgaggg	gctacccgaa	cccgcctcca	ttccctacca	480
natnntgctc	natcgggact	gacangctgg	ggatnggagg	ggctatcccc	cancatcccc	540

```

tnanaccaac agcnacngan natnggggct ccccnngggtc ggngcaacnc tctncaccc 600
cggcgcnggc cttcggtgnt gtctcctc aacnaattcc naaangggcg gccccccngt 660
ggactectcn ttgttccctc c 681

```

```

<210> 38
<211> 687
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(687)
<223> n = A,T,C or G

```

```

<400> 38
canaaaaaaa aaaacatggc cgaaaccagn aagctgcgcg atggcgccac ggccccctctt 60
ctccccggcct gtgtccggaa ggtttccctc cgagggcgccc cggtctccgc aagcggagga 120
gagggcgggga cntgcccggg ccggagctca naggccctgg ggccgctctg ctctcccgcc 180
atcgcaaggg cggcgctaac cttaggcctc cccgcaaagg tcccnangc ggngggcggcg 240
gggggctgtg anaaccgcaa aaanaacgct gggcgcgcn ggaaccgct ccccccgcg 300
aaggananac ttccacagan gcagcgtttc cacagccan agccacnttt ctagggtgat 360
gcacccagct aagttcctgn cggggaagct caccgctgtc aaaaaanctc ttcgctccac 420
cggcgcacna aggggangan ggcangangc tgccgcccgc acaggtcatc tgatcacgtc 480
gcccgccta ntctgtttt gtgaatctcc actttgttca accccaccgc ccgttctctc 540
ctccttgccg ctctctctna ccttaanaac cagcttccctc taccnatng tanttntct 600
gcncnngtng aaattaattc ggtccnccgg aacctcttnc ctgtggcaac tgctnaaaga 660
aactgctgtt ctgnttactg cngtccc 687

```

```

<210> 39
<211> 695
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(695)
<223> n = A,T,C or G

```

```

<400> 39
actagtctgg cctacaatag tgtgattcat gtaggacttc tttcatcaat tcaaaacccc 60
tagaaaaacg tatacagatt atataagtag ggataagatt tctaacattt ctgggctctc 120
tgaccctgc gctagactgt ggaaagggag tattattata gtatacaaca ctgctgttg 180
cttattagtt ataacatgat aggtgctgaa ttgtgattca caatttaaaa aactgtaat 240
ccaaactttt ttttttaact gtagatcatg catgtgaatg ttaatgttaa tttgttcaan 300
gttggttatg gtagaaaaaa ccacatgcct taaaatttta aaaagcaggg ccaaaactta 360
ttagtttaaa attaggggta tgttccagc ttgttattaa ntgggttatg ctctgtttag 420
aanaaatcna ngaacangat ttngaaantt aagntgacat tatttnccag tgacttgta 480
atttgaaatc anacacggca ccttccgttt tggtnctatt ggnntttgaa tccaancngg 540
ntccaaatct tnttggaac ngtcnntta acttttttac nanatcttat ttttttat 600
tggaatggc ctatttaang ttaaaagggg ggggnccac naccattcnt gaataaaact 660
naatatatat ccttggtccc ccaaaattta agng 695

```

```

<210> 40
<211> 674
<212> DNA

```


<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (674)

<223> n = A,T,C or G

<400> 40

actagtagtc agtgggagtg ggttgctata ccttgacttc atttatatga atttccactt	60
tattaaataa tagaaaagaa aatcccgggtg cttgcagtag agttatagga cattctatgc	120
ttacagaaaa tatagccatg attgaaatca aatagtaaag gctgttctgg ctttttatct	180
tcttagctca tcttaaataa gtagtacct tgggatgcag tgcgtctgaa gtgctaataca	240
ggttgaacaa tagcacaat cgaacttagg atgtgtttct tctcttctgt gtttcgattt	300
tgatcaattc tttaattttg ggaacctata atacagtttt cctattcttg gagataaaaa	360
ttaaatggat cactgatatt taagtcattc tgcttctcat ctnaatattc catattctgt	420
attagganaa antacctccc agcacagccc cctctcaaac cccacccaaa accaagcatt	480
tggaatgagt ctcccttatt tccgaantgt ggatgggtata acccatatcn ctccaatttc	540
tgnttgggtt ggggtattaat ttgaactgtg catgaaaagn ggnaatcttt nctttgggtc	600
aaantttncg ggttaatttg nctngncaaa tccaatttnc tttaagggtg tctttataaa	660
atttgcatt cngg	674

<210> 41

<211> 657

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (657)

<223> n = A,T,C or G

<400> 41

gaaacatgca agtaccacac actgtttgaa ttttgacaaa aaagtgactg tagggatcag	60
gtgatagccc cggaatgtac agtgtcttgg tgcaccaaga tgccttctaa aggctgacat	120
accttgggac cctaattggg cagagagtat agccctagcc cagtgggtgac atgaccactc	180
cctttgggag gctgaagtta aaggggaatgg tatgtgtttt ctcatggaag cagcacatga	240
atnggnacaa ngatgttaaa ntaaggntct antttgggtg tcttgtcatt tgaaaaantg	300
acacactcct ancanctggt aaaggggtgc tgggaagccat ggaagaactc taaaaacatt	360
agcatgggct gatctgatta cttcctggca tcccgtcac ttttatggga agtcttatta	420
naaggatggg ananttttcc atatccttgc tgttgggaact ctggaacact ctctaaattt	480
ccctctatta aaaatcactg nccttactac acttctcctc tgaanggaata gaaatggacc	540
tttctctgac ttagttcttg gcatggganc cagcccaaat taaaatctga cttntccggt	600
ttctcngaa ctcacctact tgaattggta aaacctcctt tgggaattagn aaaaacc	657

<210> 42

<211> 389

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (389)

<223> n = A,T,C or G

<400> 42

```

actagtgtctg aggaatgtaa acaagtttgc tgggccttgc gagacttcac caggttgttt      60
cgatagctca cactcctgca ctgtgcctgt caccagagaa tgtctttttt aattagaaga      120
caggaagaaa acaaaaacca gactgtgtcc cacaatcaga aacctccgtt gtggcagang      180
ggccttcacc gccaccaggg tgccccgcca gacagggaga gactccagcc ttctgaggcc      240
atcctgaaga attcctgttt gggggttgtg aaggaaaatc acccggtatt aaaaagatgc      300
tggtgcctgc ccgcgtngtn gggaaggacac tggtttcctg gtgaatttct taaaagaaaa      360
atattttaag ttaagaaaaa aaaaaaaaaa      389

```

```

<210> 43
<211> 279
<212> DNA
<213> Homo sapien

```

```

<400> 43
actagtgaca agctcctggt cttgagatgt cttctcgtaa aggagatggg ccttttgag      60
gtaaaagata aaatgaatga gttctgtcat gattcactat tctagaactt gcatgacctt      120
tactgtgtta gctctttgaa tgttcttgaa atttttagact ttctttgtaa acaaataata      180
tgtccttatc attgtataaa agctgttatg tgcaacagtg tggagatcct tgtctgattt      240
aataaaatc ttaaactg aaaaaaaaaa aaaaaaaaaa      279

```

```

<210> 44
<211> 449
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (449)
<223> n = A,T,C or G

```

```

<400> 44
actagttagca tcttttctac aacgttaaaa ttgcagaagt agcttatcat taaaaaacia      60
caacaacaac aataacaata aatcctaagt gtaaatcagt tattctaccc cctaccaagg      120
atatcagcct gttttttccc ttttttctcc tgggaataat tgtgggcttc ttcccaaatt      180
tctacagcct ctttctctt ctcattgctg agcttcctg tttgcaagca tgcgttgtgc      240
aagantgggc tggttngctt ggantncggt ccnagtggaa ncatgctttc ccttgttact      300
gttggaagaa actcaaact tcnancccta ggtgttncca ttttgtcaag tcatcactgt      360
atttttgtac tggcattaac aaaaaaagaa atnaaatatt gttccattaa actttaataa      420
aactttaaaa gggaaaaaaa aaaaaaaaaa      449

```

```

<210> 45
<211> 559
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (559)
<223> n = A,T,C or G

```

```

<400> 45
actagtgtgg gggaaatcacg gacacttaaa gtcaatctgc gaaataattc ttttattaca      60
cactcactga agttttttgag tcccagagag ccattctatg tcaaaccatt caagtactct      120
ttgagagccc agcattacat caacatgccc gtgcagttca aaccgaagtc cgcaggcaaa      180
tttgaagctt tgcttgtcat tcaaacagat gaaggcaaga gtattgctat tcgactaatt      240

```

```

ggatgaagctc ttggaaaaaa ttnactagaa tactttttgt gtttaagttaa ttacataagt 300
tgtattttgt taactttatc tttctacact acaattatgc ttttgtatat atattttgta 360
tgatggatat ctataattgt agattttgtt tttaacaagct aatactgaag actcgactga 420
aatattatgt atctagccca tagtattgta cttaactttt acaggggtgaa aaaaaaatc 480
tgtgtttgca ttgattatga tattctgaat aaatatggga atatatttta atgtgggtgaa 540
aaaaaaaaaa aaaaaggaa 559

```

```

<210> 46
<211> 731
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

```

```

<400> 46
actagttcta gtaccatggc tgtcatagat gcaaccatta tattccattt agtttcttcc 60
tcagggtccc taacaattgt ttgaaactga atatatatgt ttatgtatgt gtgtgtgttc 120
actgtcatgt atatggtgta tatgggatgt gtgcagtttt cagttatata tatattcata 180
tatacatatg catatatatg tataatatac atatatacat gcatacactt gtataatata 240
catatatata cacatatatg cacacatatn atcactgagt tccaaagtga gtcttttattt 300
ggggcaattg tattctctcc ctctgtctgc tcaactgggccc tttgcaagac atagcaattg 360
cttgatttcc tttggataag agtcttatct tcggcactct tgactctagc cttaacttta 420
gatttctatt ccagaatacc tctcatatct atcttaaaac ctaaganggg taaagangtc 480
ataagattgt agtatgaaag antttgctta gttaaattat atctcaggaa actcattcat 540
ctacaaatta aattgtaaaa tgatgggttg ttgtatctga aaaaatgttt agaacaagaa 600
atgtaactgg gtacctgtta tatcaaagaa cctcnattta ttaagtctcc tcatagccan 660
atccttatat ngccctctct gacctgantt aatananact tgaataatga atagttaatt 720
taggnnttggg c 731

```

```

<210> 47
<211> 640
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

```

```

<400> 47
tgcgngccgg tttggccctt ctttgtanga cactttcacc cgccctgaaa tcttcccgat 60
cgtaataaac tcctcaggtc cctgcctgca caggggtttt tcttantttg ttgcctaaca 120
gtacaccaa tgtgacatcc tttcaccaat atngattnct tcataccaca tcntcnatgg 180
anacgactnc aacaattttt tgatnaccn aaanactggg ggctnnaana agtacantct 240
ggagcagcat ggacctgtcn gcnactaang gaacaanagt nntgaacatt tacacaacct 300
ttggtatgtc ttactgaaag anagaaacat gcttctnncc ctagaccacg aggncaaccg 360
caganattgc caatgccaaag tccgagcggg tagatcaggg aatacattcc atggatgcat 420
tacatacnth gtccecgaaa nanaagatgc cctaanggct tcttcnact ggctcngaaa 480
acanctacac ctggtgcttg ganaacanac tctttggaag atcatctggc acaagttccc 540
cccagtggtg tttnccttgg cacctanctt accanatcna ttcggaance attctttgcc 600
ntggcnttnt nttgggacca ntcttctcac aactgnaccc 640

```

<210> 48
 <211> 257
 <212> DNA
 <213> Homo sapien

<400> 48
 actagtatat gaaaatgtaa atatcacttg tgtactcaaa caaaagtggg tcttaagctt 60
 ccaccttgag cagccttgga aacctaaccct gcctctttta gcataatcac attttctaaa 120
 tgattttctt tggtcctgaa aaagtgattt gtattagttt tacatttggt ttttggaaga 180
 ttatatgtgt atatgtatca tcataaaata tttaaataaa aagtatcttt agagtgaaaa 240
 aaaaaaaaaa aaaaaaa 257

<210> 49
 <211> 652
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (652)
 <223> n = A,T,C or G

<400> 49
 actagttcag atgagtggct gctgaagggg ccccttgctc attttcatta taaccaatt 60
 tccacttatt tgaactctta agtcataaat gtataatgac ttatgaatta gcacagttaa 120
 gttgacacta gaaactgcc atttctgtat tacactatca aataggaaac attggaaaga 180
 tggggaaaaa aatcttattt taaaatggct tagaaagttt tcagattact ttgaaaattc 240
 taaacttctt tctgtttcca aaacttgaaa atatgtagat ggactcatgc attaagactg 300
 ttttcaaagc tttcctcaca tttttaaaagt gtgattttcc ttttaataa catattttatt 360
 ttctttaaag cagctatata ccaaccatg actttggaga tatacctatn aaaccaatat 420
 aacagcangg ttattgaagc agctttctca aatgttgctt cagatgtgca agttgcaaat 480
 tttattgtat ttgtanaata caatttttgt tttaaactgt atttcaatct atttctccaa 540
 gatgcttttc atatatagtg aaatatccca ngataactgc ttctgtgtcg tcgcatttga 600
 cgcataactg cacaaatgaa cagtgtatag ctcttggttg tgcattnacc cc 652

<210> 50
 <211> 650
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (650)
 <223> n = A,T,C or G

<400> 50
 ttgcgctttg attttttttag ggcttggtgcc ctgtttcact tatagggtct agaatgcttg 60
 tgttgagtaa aaaggagatg cccaatatc aaagctgcta aatgttctct ttgccataaa 120
 gactccgtgt aactgtgtga acacttgga tttttctcct ctgtcccgag gtgcgtctct 180
 gctttctttt ttgggttctt tctagaagat tgagaaatgc atatgacagg ctgagancac 240
 ctccccaaac acacaagctc tcagccacan gcagcttctc cacagcccca gcttcgcaca 300
 ggctcctgga nggctgcctg ggggaggcag acatgggagt gccaaagtgg ccagatggtt 360
 ccaggactac aatgtcttta tttttaactg tttgccactg ctgccctcac ccctgcccg 420
 ctctggagta ccgtctgccc canacaagtg ggantgaaat gggggtggg gggaacactg 480
 attcccantt agggggtgcc taactgaaca gtagggatan aaggtgtgaa cctgngaant 540

gcttttataa attatnttcc ttgttanatt tatttttttaa tttaatctct gttnaactgc 600
ccngggaaaa ggggaaaaaa aaaaaaaaaat tctnttttaa cacatgaaca 650

<210> 51
<211> 545
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (545)
<223> n = A,T,C or G

<400> 51
tggcgtgcaa ccagggtagc tgaagtttgg gtctgggact ggagattggc cattaggcct 60
cctganattc cagctccctt ccaccaagcc cagtcttgct acgtggcaca gggcaaacct 120
gactcccttt gggcctcagt tccccctccc cttcatgana tgaaaagaat actacttttt 180
cttggttggtc taacnttgct ggacncaaag tgtngtcatt attgttgat tgggtgatgt 240
gtncaaaaact gcagaagctc actgcctatg agaggaanta agagagatag tggatganag 300
ggacanaagg agtcattatt tggtagatag ccaccntcc caacctttct ctcctcagtc 360
cctgcncctc atgtntctgg tntggtagt cctttgtgcc accanccatc atgctttgca 420
ttgctgccat cctgggaagg ggtgnatcg tctcacaact tgttgatcgc gtttganatg 480
catgctttct tnatnaaaca aanaaannaa tgtttgacag ngtttaaaat aaaaaanaaa 540
caaaa 545

<210> 52
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (678)
<223> n = A,T,C or G

<400> 52
actagtagaa gaactttgcc gcttttgtgc ctctcacagg cgcctaaagt cattgccatg 60
ggaggaagac gatttggggg gggagggggg gggggcangg tccgtggggc ttccctant 120
ntatctccat ntccantgnn cnntgtegcc tcttccctcg tcnattnga anttantccc 180
tggnccccnn nccctctccn nccnncct cccccctcg nncctccnn cttttntan 240
ncttcccat ctcntcccc cctnanngtc ccaacnccgn cagcaatnnc ncactnctc 300
nctcncnc tccnccggtt cttctnttct cnaentntnc ncnntnccn tgcnnntnaa 360
annctctccc cncgtcaanc gattctctcc ctccnccnnan ctntccactc cntncttctc 420
nncgctcct ntntctnnc ccacctctcn ccttcgnccc cantacnctc nccncccttn 480
cgnntcnttn nnntectenn accnccncc tcccttncnc cctcttctcc cgggtntntc 540
tctctccnc nncnccnct cncnccntcc nngcgnccnt ttccgcccen cncnccntt 600
ccttctcnc cantccatcn cntntnccat nctnccncc nctcacnccc gctnccccen 660
ntctctttca cacngtcc 678

<210> 53
<211> 502
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(502)
 <223> n = A,T,C or G

<400> 53
 tgaagatcct ggtgtcgcca tgggcegcgcg ccccgcccggt tgttaccggt attgtaagaa 60
 caagccgtac ccaaagtctc gcttctgcgcg aggtgtccct gatgccaaaa ttcgcatttt 120
 tgacctgggg cggaanaang caaaantgga tgagtctccg ctttgtggcc acatgggtgtc 180
 agatcaatat gagcagctgt cctctgaagc cctgnangct gcccgaattt gtgccaataa 240
 gtacatggta aaaagtngtg gcnaagatgc ttccatatcc ggggtgcgnt ccaccccttc 300
 cacgtcatcc gcatcaacaa gatgttgctc tgtgctgggg ctgacaggct cccaacaggc 360
 atgcgaagtg cctttggaaa acccanggca ctgtggccag gggttcacatt gggccaattn 420
 atcatgttca tccgcaccaa ctgcagaaca angaacntgt naattnaagc cctgcccagg 480
 gncaanttca aatttcccgc cc 502

<210> 54
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 54
 actagtccaa gaaaaatatg cttaatgtat attacaaagg ctttgtatat gttaacctgt 60
 tttaatgcca aaagtttgct ttgtccacaa tttccttaag acctcttcag aaagggattt 120
 gtttgcccta atgaatactg ttgggaaaaa acacagtata atgagtgaag agggcagaag 180
 caagaaattt ctacatctta gcgactccaa gaagaatgag tatccacatt tagatggcac 240
 attatgagga ctttaattctt tccttaaaaca caataatgtt ttcttttttc ttttattcac 300
 atgatttcta agtatatttt tcatgcagga cagtttttca accttgatgt acagtgactg 360
 tgttaaattt ttctttcagt ggcaacctct ataatcttta aaatatgggt agcatcttgt 420
 ctgttttgaa ngggatatga cnatnaatct atcagatggg aaatcctgtt tccaagttag 480
 aaaaaaaaaa aaaa 494

<210> 55
 <211> 606
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(606)
 <223> n = A,T,C or G

<400> 55
 actagtaaaa agcagcattg ccaaataatc cctaattttc cactaaaaat ataatgaaat 60
 gatgttaagc tttttgaaaa gtttaggtta aacctactgt tgtagatta atgtatttgt 120
 tgcttcctt tatctggaat gtggcattag cttttttatt ttaacctct ttaattctta 180
 ttcaattcca tgacttaagg ttggagagct aaacactggg atttttggat aacagactga 240
 cagttttgca taattataat cggcattgta catagaaagg atatggctac cttttgttaa 300
 atctgcactt tctaaatatc aaaaaaggga aatgaagtat aaatcaattt ttgtataatc 360
 tgtttgaaac atgantttta tttgcttaat attanggctt tgcccttttc tgttagtctc 420
 ttgggacccg gtgtaaaact gttctcatta aacaccaaac agttaagtc attctctggg 480

```

actagctaca aattccgttt catattctac ntaacaattt aaattaactg aaatatttct 540
anatggtcta cttctgtcnt ataaaaacna aacttgantt nccaaaaaaa aaaaaaaaaa 600
aaaaaa 606

```

```

<210> 56
<211> 183
<212> DNA
<213> Homo sapien

```

```

<400> 56
actagtatat ttaaacttac aggcttattt gtaatgtaaa ccaccatttt aatgtactgt 60
aattaacatg gttataatac gtacaatcct tccctcatcc catcacacaa ctttttttgt 120
gtgtgataaa ctgattttgg tttgcaataa aaccttgaaa aataaaaaaa aaaaaaaaaa 180
aaa 183

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```

<210> 57
<211> 622
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (622)
<223> n = A,T,C or G

```

```

<400> 57
actagtcact actgtcttct ccttgtagct aatcaatcaa tattcttccc ttgcctgtgg 60
gcagtggaga gtgctgctgg gtgtacgctg cacctgcccc ctgagttggg gaaagaggat 120
aatcagtgag cactgttctg ctcagagctc ctgatctacc ccacccccta ggatccagga 180
ctgggtcaaa gctgcatgaa accaggccct ggcagcaacc tgggaatggc tggaggtggg 240
agagaacctg acttctcttt cctctctcct cctccaacat tactggaact ctatcctgtt 300
agggatcttc tgagcttgtt tccctgctgg gtgggacaga agacaaagga gaagggangg 360
tctacaanaa gcagcccttc tttgtcctct ggggttaatg agcttgacct ananttcag 420
gaganaccan aagcctctga tttttaattt ccntnaaatg tttgaagtnt atatntacat 480
atatatattt ctttnaatnt ttgagtcttt gatatgtctt aaaatccant ccctctgccn 540
gaaacctgaa ttaaaacat gaanaaaaat gtttncctta aagatgttan taattaattg 600
aaacttgaaa aaaaaaaaaa aa 622

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<210> 58
<211> 433
<212> DNA
<213> Homo sapien

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<400> 58
gaacaaattc tgattggtta tgtaccgtca aaagacttga agaaatttca tgattttgca 60
gtgtggaagc gttgaaaatt gaaagttact gcttttccac ttgctcatat agtaaaggga 120
tcctttcagc tgccagtgtt gaataatgta tcatccagag tgatgttatc tgtgacagtc 180
accagcttta agctgaacca ttttatgaat accaaataaa tagacctctt gtactgaaaa 240
catattttgt actttaatcg tgctgcttgg atagaaatat ttttactggg tcttctgaat 300
tgacagtaaa cctgtccatt atgaatggcc tactgttcta ttatttgttt tgacttgaat 360
ttatccacca aagacttcat ttgtgtatca tcaataaagt tgtatgtttc aactgaaaaa 420
aaaaaaaaa aaa 433

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<210> 59
<211> 649

```

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(649)
<223> n = A,T,C or G

<400> 59
actagttatt atctgacttt cngggtataa tcattctaata gagtgtgaag tagcctctgg 60
tgtcatttgg atttgcattt ctctgatgag tgatgctatc aagcaccttt gctgggtgctg 120
ttggccatat gtgtatgttc cctggagaag tgtctgtgct gagccttggc ccacttttta 180
attaggcgtt tgtcttttta ttactgagtt gtaaganttc tttatatatt ctggattcta 240
gacccttatc agatacatgg ttgcaataa tttctccca ttctgtgggt tgtgttttca 300
ctttatcgat aatgtcctta gacatataat aaatttgtat tttaaaagtg acttgatttg 360
ggctgtgcaa ggtgggctca cgcttgtaat ccagcactt tgggagactg aggtgggtgg 420
atcatatgan gangctagga gtctgaggtc agcctggcca gcatagcgaa aacttgtctc 480
tacnaaaat acaaaaatta gtcaggcatg gtggtgcacg tctgtaatac cagcttctca 540
ggangctgan gcacaaggat cacttgaacc ccagaangaa gangttgcag tganctgaag 600
atcatgccag ggcaacaaaa atgagaactt gttaaaaaa aaaaaaaaaa 649

<210> 60
<211> 423
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(423)
<223> n = A,T,C or G

<400> 60
actagttcag gccttcagtc tcaactgacaa acatggggaa gtgtgcccag ctggctggaa 60
acctggcagt gataccatca agcctgatgt ccaaaagagc aaagaatatt tctccaagca 120
gaagtgagcg ctgggctgtt ttagtgccag gctgcggtgg gcagccatga gaacaaaacc 180
tcttctgtat ttttttttct cattagtgana acacaagact cngattcagc cgaattgtgg 240
tgtcttaciaa ggcagggcct tcctacaggg ggtggananaa acagccttct ttcctttggt 300
aggaatggcc tgagttggcg ttgtgggcag gctactggtt tgtatgatgt attagtagag 360
caaccattta atcttttcta gtttctatna aacttganct gagaccttaa aaaaaaaaaa 420
aaa 423

<210> 61
<211> 423
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(423)
<223> n = A,T,C or G

<400> 61
cgggactgga atgtaaagtg aagttcggag ctctgagcac gggtcttctc cgccgggtcc 60
tccctcccca gacccagag ggagaggccc accccgcccc gccccgcccc agccctgtct 120
caggtctgag tatggctggg agtcgggggc cacaggcctc tagctgtgct gctcaagaag 180

actggatcag	ggtanctaca	agtggccggg	ccttgccctt	gggattctac	cctgttccta	240
atttgggtgt	ggggtgcggg	gtccctggcc	cccttttcca	cactnccctc	ctccngacag	300
caacctccct	tggggcaatt	gggcctggnt	ctccncccg	tgttgcnaac	ctttgttggt	360
ttaaggncct	taaaaatggt	annttttccc	ntgcncgggt	taaaaaagga	aaaaactnaa	420
aaa						423

<210> 62
 <211> 683
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (683)
 <223> n = A,T,C or G

<400> 62						
gctggagagg	ggtacggact	ttcttgagg	tgtcccaggt	tggaatgaga	ctgaactcaa	60
gaagagaccc	taagagactg	gggaatgggt	cctgccttca	ggaaagtga	agacgcttag	120
gctgtcaaca	cttaaaggaa	gtccccttga	agcccagagt	ggacagacta	gacccattga	180
tggggccact	ggccatgggc	cgtggacaag	acattccngt	gggccatggc	acaccggggg	240
ggatcaaaat	gtgtacttgt	ggggtctcgc	cccttgccaa	aaccaaacca	ntcccactcc	300
tgtcnttgga	ctttcttccc	attccctcct	ccccaaatgc	acttcccctc	ctccctctgc	360
ccctcctgtg	tttttggaat	tctgtttccc	tcaaaattgt	taatttttta	nttttngacc	420
atgaacttat	gtttgggggc	nangttcccc	tnccaatgc	atactaatat	attaatgggt	480
atztattttt	gaaatatatt	ttaatgaact	tggaaaaaat	tnntggaatt	tccttncttc	540
cntttntttt	gggggggggtg	gggggntggg	ttaaaatttt	tttggaancc	cnatnggaaa	600
ttnttacttg	gggccccct	naaaaaantn	anttccaatt	cttnnatngc	ccctnttccn	660
ctaaaaaaaa	ananannaaa	aan				683

<210> 63
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (731)
 <223> n = A,T,C or G

<400> 63						
actagtcata	aagggtgtgc	gcgtcttcga	cgtggcggtc	ttggcgccac	tgctgcgaga	60
cccggccctg	gacctcaagg	tcatecaatt	ggtgcgtgat	ccccgcgcgg	tggcgagttc	120
acggatccgc	tcgcgccacg	gcctcatccg	tgagagccta	cagggtggtgc	gcagccgaga	180
ccgcgagctc	accgcatgcc	cttcttgagg	gccgcggggc	acaagcttgg	cgcccaaaaa	240
gaaggcgtn	ggggcccgca	aantaccacg	ctctgggcgc	tatggaangt	cctcttgcaa	300
taatattggt	tnaaaantcg	canaanagcc	cctgcancct	cctgaactgg	gntgcagggc	360
cncttacctn	gtttggntgc	ggttacaaa	aacctgtttn	ggaaaaccct	nccnaaaacc	420
ttccgggaaa	attntncaaa	ttttnttgg	ggaattnttg	ggtaaaccct	ccnaaaatgg	480
gaaacntttt	tgccctnnaa	antaaacat	tnngttccgg	gggccccccc	ncaaaaccct	540
ttttnttttt	ttntgcccc	cantnncccc	ccggggcccc	tttttttngg	ggaaaanccc	600
ccccctncc	nanantttta	aaaggngggg	anaatttttn	nttncccccc	gggncccccn	660
ggngntaaaa	nggtttcncc	cccccgaggg	gngggggnnc	ctcnnaaacc	cntntcnna	720
ccncttttn	n					731

<210> 64
 <211> 313
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(313)
 <223> n = A,T,C or G

<400> 64
 actagttgtg caaaccacga ctgaagaaag acgaaaagtg ggaaataact tgcaacgtct 60
 gttagagatg gttgctacac atgttgggtc tgtagagaaa catcttgagg agcagattgc 120
 taaagttgat agagaatatg aagaatgcat gtcagaagat ctctcggaaa atattaaaga 180
 gattagagat aagtatgaga agaaagctac tctaattaag tcttctgaag aatgaagatn 240
 aaatgttgat catgtatata tatccatagt gaataaaatt gtctcagtaa agttgtaaaa 300
 aaaaaaaaaaaa aaa 313

<210> 65
 <211> 420
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(420)
 <223> n = A,T,C or G

<400> 65
 actagttccc tggcaggcaa gggcttccaa ctgaggcagt gcatgtgtgg cagagagagg 60
 caggaagctg gcagtggcag cttctgtgtc tagggagggg tgtggctccc tcttccctg 120
 tctgggaggt tggagggaag aatctaggcc ttagcttgcc ctctgccac ccttcccctt 180
 gtagatactg ccttaacact ccctcctctc tcagctgtgg ctgccacca agccagggtt 240
 ctccgtgctc actaatttat ttccaggaaa ggtgtgtgga agacatgagc cgtgtataat 300
 atttgtttta acattttcat tgcaagtatt gaccatcatc cttgggtgtg tatcgttgta 360
 acacaaatta atgatattaa aaagcatcca aacaaagccn annnnnaana nnannngaaa 420

<210> 66
 <211> 676
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(676)
 <223> n = A,T,C or G

<400> 66
 actagtttcc tatgatcatt aaactcatte tcagggttaa gaaaggaatg taaatttctg 60
 cctcaatttg tacttcatca ataagttttt gaagagtgcg gatttttagt caggtcttaa 120
 aaataaaact acaaactctg atgcatttct aaattctgca aatgtttcct ggggtgactt 180
 aacaaggaat aatcccacaa tatacttagc tacctaatac atggagctgg ggctcaaccc 240
 actgttttta aggatttgcg cttacttgtg gctgaggaaa aataagtagt tccgagggaa 300
 gtagttttta aatgtgagct tatagatngg aaacagaata tcaacttaat tatggaaatt 360
 gtagaaaacc tgttctcttg ttatctgaat cttgattgca attactattg tactggatag 420

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actccagccc attgcaaagt ctcagatatc ttanctgtgt agttgaattc cttggaaatt 480
ctttttaaga aaaaattgga gtttnaaaga aataaacccc tttgttaaata gaagcttggc 540
tttttggtga aaaanaatca tcccgcaggg cttattgttt aaaaanggaa ttttaagcct 600
ccctggaaaa anttgттаат taaatgggga aaatgntggg naaaaattat ccgttagggt 660
ttaaaggga aactta 676

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<210> 67
<211> 620
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1) ... (620)
<223> n = A,T,C or G

```

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<400> 67
caccattaaa gctgcttacc aagaacttcc ccagcatttt gacttccttg tttgatagct 60
gaattgtgag cagggtgatag aagagccttt ctagttgaac atacagataa tttgctgaat 120
acattccatt taatgaagg gttacatctg ttacgaagct actaagaagg agcaagagca 180
taggggaaaa aaatctgac agaacgcac aaactcacat gtgccccctc tactacaaac 240
agattgtagt gctgtggtgg tttattccgt tgtgcagaac ttgcaagctg agtcactaaa 300
cccaaagaga ggaaattata ggtagttaa acattgtaat ccaggaact aagtttaatt 360
cacttttgaa gtgttttggt tttattttt ggttgtctg atttactttg ggggaaaang 420
ctaaaaaaaa agggatatca atctctaatt cagtgcccac taaaagttgt ccctaaaaag 480
tctttactgg aanttatggg actttttaag ctccaggtnt tttggtcctc caaattaacc 540
ttgcatgggc cccttaaaat tgtgaangg cattcctgcc tctaagtttg gggaaaattc 600
ccccntttt aaaaatttga 620

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<210> 68
<211> 551
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1) ... (551)
<223> n = A,T,C or G

```

```

<400> 68
actagtagct ggtacataat cactgaggag ctatttctta acatgctttt atagaccatg 60
ctaagtctag accagtattt aagggtctaat ctcacacctc cttagctgta agagtctggc 120
ttagaacaga cctctctgtg caataacttg tggccactgg aaatccctgg gccggcattt 180
gtattggggt tgcaatgact cccaagggcc aaaagagtta aaggcacgac tgggatttct 240
tctgagactg tggtgaaact cctccaagg ctgagggggt cagtangtgc tctgggaggg 300
actcggcacc actttgatat tcaacaagcc acttgaagcc caattataaa attgttattt 360
tacagctgat ggaactcaat ttgaaccttc aaaactttgt tagtttatcc tatttatattg 420
ttaaacctaa ttacatttgt ctagcattgg atttggttcc tgtngcatat gtttttttcn 480
cctatgtgct cccctcccc nnatcttaat ttaaacnca attttgcnat tcncnnnnnn 540
nannnnanna a 551

```

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<210> 69
<211> 396
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)... (396)
 <223> n = A,T,C or G

<400> 69
 cagaaatgga aagcagagtt ttcatttctg tttataaacg tctccaaaca aaaatggaaa 60
 gcagagtttt cattaaatcc ttttaccttt tttttttctt ggtaatcccc tcaaataaca 120
 gtatgtggga tattgaatgt taaaggata tttttttcta ttatttttat aattgtacaa 180
 aattaagcaa atgttaaaag ttttatatgc tttattaatg ttttcaaaag gtatnataca 240
 tgtgatacat tttttaagct tcagttgctt gtcttctggt actttctggt atgggctttt 300
 ggggagccan aaaccaatct acnatctctt tttgtttgcc aggacatgca ataaaattta 360
 aaaaataaat aaaaactatt nagaaattga aaaaaa 396

<210> 70
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (536)
 <223> n = A,T,C or G

<400> 70
 actagtgcga aagcaaatat aaacatcgaa aaggcggttcc tcacgttagc tgaagatata 60
 cttcgaaaga cccctgtaaa agagcccaac agtgaaaatg tagatatcag cagtggagga 120
 ggcgtgacag gctggaagag caaatgctgc tgagcattct cctgttccat cagttgccat 180
 ccactacccc gttttctctt cttgctgcaa aataaaccac tctgtccatt tttaactcta 240
 aacagatatt tttgtttctc atcttaacta tccaagccac ctattttatt tgttctttca 300
 tctgtgactg cttgctgact ttatcataat tttcttcaaa caaaaaaatg tatagaaaaa 360
 tcatgtctgt gacttcattt ttaaatgnta cttgctcagc tcaactgcat ttcagttggt 420
 ttatagtcca gttcttatca acattnaaac ctatngcaat catttcaaat ctattctgca 480
 aattgtataa gaataaaaagt tagaatttaa caattaaaaa aaaaaaaaaa aaaaaa 536

<210> 71
 <211> 865
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (865)
 <223> n = A,T,C or G

<400> 71
 gacaaagcgt taggagaaga anagaggcag ggaanactnc ccaggcacga tggccncctt 60
 cccaccagca accagcgcgc cccaccagcc cccaggcccg gacgacgaag actccatcct 120
 ggattaatct nacctctntc gcctgnccca ttcctacctc ggaggtggag gccggaaagg 180
 tcncaccaag aganaantcg ctgccaacac caaccgcccc agccctggcg ggcacganag 240
 gaaactggtg accaatctgc agaattctna gaggaanaag cnaggggccc cgcgctnaga 300
 cagagctgga tatgangcca gaccatggac nctacnccn ncaatncana cgggactgcy 360
 gaagatggan gaccncgcac nngatcaggc cngctnncca nccccccacc cctatgaatt 420
 attcccgctg aangaatctc tgannggctt ccannaaagc gcctccccnc cnaacgnaan 480

tncaacatng	ggattanang	ctgggaactg	naaggggcaa	ancctnnaat	atccccagaa	540
acaanctctc	ccnaanaaac	tggggcncct	catnggtggn	accaactatt	aactaaaccg	600
cacgccaagn	aantataaaa	ggggggcccc	tcnccggngg	accccctttt	gtcccttaat	660
ganggttatc	cnccttgctg	accatggtn	ccnnttctgt	ntgnatgttt	ccnctccctt	720
ccncttatnt	cnagccgaac	tcnnattnnc	ccgggggtgc	natcnantng	tncncttttn	780
ttngttgncc	cngecccttc	cgncgggaacn	cgtttccccg	ttantaacgg	caccgggggn	840
aagggtgntt	ggccccctcc	ctccc				865

<210> 72

<211> 560

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(560)

<223> n = A,T,C or G

<400> 72

cctggacttg	tcttggttcc	agaacctgac	gacccggcga	cgggcgacgtc	tcttttgact	60
aaaagacagt	gtccagtgtc	ccngcctagg	agtctacggg	gaccgcctcc	cgcgcgcgcca	120
ccatgcccac	cttctctggc	aactggaaaa	tcattccgatc	ggaaaacttc	gangaattgc	180
tcnaantgct	gggggtgaat	gtgatgctna	ngaanattgc	tgtggctgca	gcgtccaagc	240
cagcagtggg	gatcnaacag	gagggagaca	ctttctacat	caaaaacctcc	accacctgtc	300
gcaccacaaa	gattaacttc	nnngttgggg	aggantttga	ggancaaact	gtggatngga	360
ngcctgtnaa	aacctggtga	aatgggagaa	tganaataaa	atgggtctgtg	ancanaaact	420
cctgaaayga	gaaggccccc	anaactcctg	gaccngaaaa	actgaccnc	cnatngggga	480
actgatnctt	gaacctgaa	cgggcgggat	ganccttttt	tnttgccncc	naanggggtc	540
tttccttttc	cccaaaaaaa					560

<210> 73

<211> 379

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 73

ctggggancc	ggcggtnggc	nccatntcnn	gncgcgaagg	tggcaataaa	aanccnctga	60
aaccgcncac	naaacatgcc	naagatatgg	acgaggaaga	tnngcttttc	nngnacaanc	120
gnannagagga	acanaacaaa	ctcnangagc	tctcaagcta	atgccgcggg	gaagggggccc	180
ttggccacnn	gtggaattaa	gaaatctggc	aaanngtann	tgttccttgt	gcctnangag	240
ataagnagcc	ctttatttca	tctgtattta	aacctctctn	ttccctgnca	taacttcttt	300
tnccacgtan	agntggaant	anttgtgtgc	ttggactgtt	gtncatttta	gannaaactt	360
ttgttcaaaa	aaaaaataa					379

<210> 74

<211> 437

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(437)
 <223> n = A,T,C or G

<400> 74
 actagttcag actgccacgc caaccccaga aaatacccca catgccagaa aagtgaagtc 60
 ctagggtgttt ccattctatgt ttcaatctgt ccattctacca ggcctcgga taaaaacaaa 120
 acaaaaaaac gctgccaggt ttanaagca gttctggtct caaaaccatc aggatcctgc 180
 caccagggtt cttttgaaat agtaccacat gtaaaaggga atttggttt cacttcattct 240
 aatcactgaa ttgtcaggct ttgattgata attgtagaaa taagtagcct tctgttggtg 300
 gaataagtta taatcagtat tcatctcttt gttttttgtc actcttttct ctctnattgt 360
 gtcatattgta ctgtttgaaa aatatttctt ctataaaatt aaactaacct gccttaaaaa 420
 aaaaaaaaaa aaaaaaa 437

<210> 75
 <211> 579
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(579)
 <223> n = A,T,C or G

<400> 75
 ctccgtcgcc gccaaagatga tgtgcggggc gccctccgcc acgcagccgg ccaccgccga 60
 gaccagcac atcgccgacc aggtgaggtc ccagcttgaa gagaaagaaa acaagaagtt 120
 ccctgtgttt aaggccgtgt cattcaagag ccagggtggtc gcggggacaa actacttcat 180
 caagggtgcac gtcggcgacg aggtctcgt acacctgcga gtgttccaat ctctccctca 240
 tgaatacaag cccttgacct tatctaacta ccagaccaac aaagccaagc atgatgagct 300
 gacctatttc tgatcctgac ttgggacaag gcccttcagc cagaagactg acaagtcatt 360
 cctccgtcta ccagagcgtg cacttgatgat cctaaaataa gcttcattctc cgggctgtgc 420
 ccttggggtg gaaggggcan gatctgcact gcttttgcat ttctcttctt aaatttcatt 480
 gtgttgattc ttctcttcca ataggtgatc ttnattactt tcagaatatt ttccaaatna 540
 gatataattt naaaatcctt aaaaaaaaaa aaaaaaaaaa 579

<210> 76
 <211> 666
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(666)
 <223> n = A,T,C or G

<400> 76
 gttttatccta tctctccaac cagattgtca gctccttgag ggcaagagcc acagtatatt 60
 tccctgtttc ttccacagtg cctaataata ctgtggaact aggttttaaat aattttttta 120
 ttgatgttgt tatgggcagg atggcaacca gaccattgtc tcagagcagg tgctggctct 180
 ttcttggtca ctccatgttg gctagcctct ggtaacctct tacttattat cttcaggaca 240
 ctactacag ggaccaggga tgatgcaaca tccttgctct tttatgacag gatgtttgct 300
 cagcttctcc aacaataaaa agcacgtggt aaaacacttg cggatattct ggactgtttt 360
 taaaaaatat acagtttacc gaaaatcata ttatcttaca atgaaaagga ntttatagat 420
 cagccagtga acaacctttt cccaccatac aaaaattcct tttcccgaan gaaaanggct 480

ttctcaataa	ncctcacttt	cttaanatct	tacaagatag	ccccganatc	ttatcgaaac	540
tcatttttagg	caaatatgan	ttttattgtg	cgttacttgt	ttcaaaat	gggtattgtga	600
atatcaatta	ccacccccat	ctcccatgaa	anaaanggga	aanggtgaan	ttcntaancg	660
cttaaa						666

<210> 77

<211> 396

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(396)

<223> n = A,T,C or G

<400> 77

ctgcagccccg	ggggatccac	taatctacca	nggttatttg	gcagctaatt	ctanatttgg	60
atcattgccc	aaagttgcac	ttgctggtct	cttgggattt	ggccttgga	aggtatcata	120
catanganta	tgccanaata	aattccattt	ttttgaaaat	canctcctg	gggctgggtt	180
tggtccacag	cataacangc	actgcctcct	tacctgtgag	gaatgcaaaa	taaagcatgg	240
attaagttag	aaggagact	ctcagccttc	agcttcctaa	attctgtgtc	tgtgactttc	300
gaagtttttt	aaacctctga	atttgtacac	atttaaaatt	tcaagtgtac	tttaaaataa	360
aatacttcta	atgggaacaa	aaaaaaaaaa	aaaaaa			396

<210> 78

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(793)

<223> n = A,T,C or G

<400> 78

gcacccctagc	cgccgactca	cacaaggcag	gtgggtgagg	aaatccagag	ttgccatgga	60
gaaaattcca	gtgtcagcat	tcttgctcct	tgtggccctc	tcctacactc	tgccagaga	120
taccacagtc	aaacctggag	ccaaaaagga	cacaaaggac	tctcgaccca	aactgcccc	180
gacctctctc	agaggttggg	gtgaccaact	catctggact	cagacatatg	aagaagctct	240
atataaatcc	aagacaagca	acaaaccctt	gatgattatt	catcacttgg	atgagtggcc	300
acacagtcna	gctttaaaga	aagtgtttgc	tgaaaataaa	gaaatccaga	aattggcaga	360
gcagtttgtc	ctcctcaatc	tggtttatga	aacaactgac	aaacaccttt	ctcctgatgg	420
ccagtattgtc	ccaggattat	gtttgttgac	ccatctctga	cagttgaagc	cgatatcctg	480
ggaagatatt	cnaaccgtct	ctatgcttac	aaactgcaga	tacgtctctg	tgcttgacac	540
atgaaaaagc	tctcaagttg	ctnaaaatga	attgtaagaa	aaaaaatctc	cagccttctg	600
tctgtcggct	tgaaaattga	aaccagaaaa	atgtgaaaaa	tggtctattg	ggaacanatn	660
gacacctgat	taggttttgg	ttatgttcac	cactattttt	aanaaaanan	nttttaaaat	720
ttggttcaat	tntctttttn	aaacaatntg	tttctacntt	gnganctgat	ttctaaaaaa	780
aataatnttt	ggc					793

<210> 79

<211> 456

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(456)

<223> n = A,T,C or G

<400> 79

actagtatgg ggtgggaggc cccacccttc tcccctagge gctgttcttg ctccaaaggg	60
ctccgtggag agggactggc agagctgang ccacctgggg ctggggatcc cactcttctt	120
gcagctgttg agcgcaccta accactggtc atgccccac ccctgctctc cgcacccgct	180
tcctcccgac cccangacca ggctacttct cccctcctct tgcctccctc ctgcccctgc	240
tgcctctgat cgtangaatt gangantgtc ccgccttggt gctganaatg gacagtggca	300
ggggctggaa atgggtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcnccccc	360
tgcaagaccg agattgaggg aaancatgtc tgctgggtgt gaccatgttt cctctccata	420
aantnccct gtgacnctca naaaaaaaaa aaaaaa	456

<210> 80

<211> 284

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(284)

<223> n = A,T,C or G

<400> 80

ctttgtacct ctagaaaaga taggtattgt gtcatgaaac ttgagttaa attttatata	60
taaaactaaa agtaatgtc acttttagcaa cacatactaa aattggaacc atactgagaa	120
gaatagcatg acctccgtgc aaacaggaca agcaaatttg tgatgtgttg attaaaaaga	180
aataaataaa tgtgtatatg tgtaacttgt atgtttatgt ggaatacaga ttgggaaata	240
aaatgtattt cttactgtga aaaaaaaaa aaaaaaaaa aana	284

<210> 81

<211> 671

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(671)

<223> n = A,T,C or G

<400> 81

gccaccaaca ttccaagcta ccctgggtac ctttgtgcag tagaagctag tgagcatgtg	60
agcaagcggg gtgcacacgg agactcatcg ttataattta ctatctgcca agagtagaaa	120
gaaaggctgg ggatatttgg gttggcttgg ttttgatttt ttgcttgttt gtttgtttt	180
tactaaaaa gtattatctt ttgaatatcg tagggacata agtatataca tgttatccaa	240
tcaagatggc tagaatgggt cctttctgag tgtctaaaac ttgacacccc tggtaaatct	300
ttcaacacac ttccactgcc tgcgtaatga agttttgatt catttttaac cactggaatt	360
tttcaatgcc gtcattttca gttagatnat tttgcacttt gagattaaaa tgccatgtct	420
atttgattag tcttattttt ttatttttac aggcattatca gtctcactgt tggtgtcat	480
tgtgacaaag tcaaataaac ccccnaggac aacacacagt atgggatcac atattgtttg	540
acattaagct ttggccaaaa aatggtgcat gtgttttacc tcgacttgct aaatcaatan	600
canaaaggct ggctnataat gttggtggtg aaataattaa tnantaacca aaaaaaaaa	660
aaaaaaaaa a	671

<210> 82
 <211> 217
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(217)
 <223> n = A,T,C or G

<400> 82
 ctgcagatgt ttcttgaatg ctttgtcaaa ttaanaaagt taaagtgcaa taatgtttga 60
 agacaataag tgggtggtgta tcttgtttct aataagataa acttttttgt ctttgcctta 120
 tcttattagg gagttgtatg tcagtgata aaacatactg tgtggtataa caggcttaat 180
 aaattcctta aaaggaaaaa aaaaaaaaaa aaaaaaa 217

<210> 83
 <211> 460
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(460)
 <223> n = A,T,C or G

<400> 83
 cgcgagtggg agcaccagga tctcgggctc ggaacgagac tgcacggatt gttttaagaa 60
 aatggcagac aaaccagaca tgggggaaat cgccagcttc gatnaggcca agctgaanaa 120
 aacggagacg caggagaaga acaccctgcc gaccaaagag accattgagc angagaagcg 180
 gagtgaatt tcctaagatc ctggaggatt tcctaccccc gtctctctcg agaccccagt 240
 cgtgatgtgg aggaagagcc acctgcaaga tggacacgag ccacaagctg cactgtgaac 300
 ctgggcactc cgcgccgatg ccaccggcct gtgggtctct gaagggaccc cccccaatcg 360
 gactgcaaaa ttctccggtt tgccccggga tattatacaa nattatttgt atgaataatg 420
 annataaaac acacctcgtg gcancaana aaaaaaaaaa 460

<210> 84
 <211> 323
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(323)
 <223> n = A,T,C or G

<400> 84
 tgggtgatct tggctctgtg gagctgctgg gacgggatct aaaagactat tctggaagct 60
 gtggtccaan gcattttgct ggcttaacgg gtcccggaac aaaggacacc agctctctaa 120
 aattgaagtt taccganat aacaatcttt tgggcagaga tgcctatttt aacaaacncc 180
 gtccctgcgc aacaacnaac aatctctggg aaataccggc catgaacntg ctgtctcaat 240
 cnancatctc tctagctgac cgatcatatc gtcccagatt actacanatc ataataattg 300
 atttcctgta naaaaaaaaa aaa 323

<210> 85
<211> 771
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (771)
<223> n = A,T,C or G

<400> 85
aaactgggta ctcaacactg agcagatctg ttctttgagc taaaaacccat gtgctgtacc 60
aanagtttgc tcctggctgc tttgatgtca gtgctgtctac tccacctctg cggcgaatca 120
gaagcaagca actttgactg ctgtcttgga tacacagacc gtattcttca tcctaaatctt 180
attgtgggct tcacacggca gctggccaat gaaggctgtg acatcaatgc tatcatcttt 240
cacacaaaaga aaaagtgtgc tgtgtgcgca aatccaaaac agacttgggt gaaatatatt 300
gtgctgtctcc tcagtaaaaa agtcaagaac atgtaaaaac tgtggctttt ctggaatgga 360
attggacata gcccaagaac agaaagaact tgctgggggt ggagggtttca cttgcacatc 420
atgganggtt tagtgcttat cttattttgt cctcctggac ttgtccaatt natgaagtta 480
atcatattgc atcatanttt gctttgttta acatcacatt naaattaaac tgtattttat 540
gttatttata gctntaggtt ttctgtgttt aactttttat acnaantttc ctaaaactatt 600
ttggtntant gcaanttaaa aatttatattt ggggggggaa taaatatttg antttctgca 660
gccacaagct ttttttaaaa aaccantaca nccnngtta atggtnggtc ccnaatggtt 720
tttgcttttn antagaaaat ttnttagaac natttgaaaa aaaaaaaaaa a 771

<210> 86
<211> 628
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (628)
<223> n = A,T,C or G

<400> 86
actagtttgc tttacatttt tgaaaagtat tatttttgtc caagtgttta tcaactaaac 60
cttgtgttag gtaagaatgg aatttattaa gtgaatcagt gtgacccttc ttgtcataag 120
attatcttaa agctgaagcc aaaatatgct tcaaaagaaa angactttat tgttcattgt 180
agttcatata ttcaaagcat ctgaactgta gtttctatag caagccaatt acatccataa 240
gtggagaang aaatagatta atgtcnaagt atgattgggt gagggagcaa ggttgaagat 300
aatctggggt tgaaattttc tagttttcat tctgtacatt tttagttnga catcagattt 360
gaaatattaa tgtttacctt tcaatgtgtg gtatcagctg gactcantaa caccctttc 420
ttccctnngg gatggggaat ggattattgg aaaatggaaa gaaaaaagta cttaaagcct 480
tcctttcnca gtttctggct cctaccctac tgatttancc agaataagaa aacattttat 540
catcntctgc tttattccca ttaatnaant tttgatgaat aaatctgctt ttatgcnnac 600
ccaaggaatt nagtggnntc ntcnttgt 628

<210> 87
<211> 518
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(518)

<223> n = A,T,C or G

<400> 87

ttttttattt	tttttagaga	gtagttcagc	ttttatttat	aaattttattg	cctgtttttat	60
tataacaaca	ttatactgtt	tatggtttaa	tacatatggg	tcaaaatgta	taatacatca	120
agtagtacag	ttttaaaatt	ttatgcttaa	aacaagtttt	gtgtaaaaaa	tgagatata	180
ttttacatgg	caaatcaatt	tttaagtcac	cctaaaaaatt	gatttttttt	tgaaatttaa	240
aaacacattt	aattttcaatt	tctctcttat	ataaccttta	ttactatagc	atggtttcca	300
ctacagttta	acaatgcagc	aaaattccca	tttcacggta	aattgggttt	taagcggcaa	360
ggttaaaatg	ctttgaggat	cctnaatacc	ctttgaaatt	caaatgaagg	ttatgggtgt	420
naatttaacc	ctcatgccat	aagcagaagc	acaagtttag	ctgcattttg	ctctaaactg	480
taaaancgag	ccccccgttg	aaaaagcaaa	agggaccc			518

<210> 88

<211> 1844

<212> DNA

<213> Homo sapien

<400> 88

gagacagtga	atcctagtat	caaaggattt	ttggcctcag	aaaaagttgt	tgattatttt	60
tattttattt	tatttttcga	gactccgtct	caaaaaaaaa	aaaaaaaaaa	agaatcacaa	120
ggtagttgct	aaagcatttt	gagctgcttg	gaaaaaggga	agtagttgca	gtagagtttc	180
ttccatcttc	ttgggtgctg	gaagccatat	atgtgtcttt	tactcaagct	aaggggtata	240
agcttatgtg	ttgaatttgc	tacatctata	tttcacatat	tctcacaata	agagaatttt	300
gaaatagaaa	tatcatagaa	catttaagaa	agtttagtat	aaataatatt	ttgtgtgttt	360
taatcccttt	gaagggatct	atccaaagaa	aatattttac	actgagctcc	ttcctacacg	420
tctcagtaac	agatcctgtg	ttagtctttg	aaaatagctc	attttttaaa	tgtagtgag	480
tagatgtagc	atacatatga	tgtataatga	cgtgtattat	gttaacaatg	tctgcagatt	540
ttgtaggaat	acaaaacatg	gcctttttta	taagcaaaac	gggccaatga	ctagaataac	600
acatagggca	atctgtgaat	atgtattata	agcagcattc	cagaaaagta	gttgggtgaa	660
taattttcaa	gtcaaaaagg	gatatggaaa	gggaattatg	agtaacctct	attttttaag	720
ccttgctttt	aaattaaacg	ctacagccat	tttagccttg	aggataataa	agcttgagag	780
taataatggt	agggttagcaa	agggttagat	gtatcacttc	atgcatgcta	ccatgatagt	840
aatgcagctc	ttcgagtcac	ttctgggtcat	tcaagatatt	cacccttttg	cccatagaaa	900
gcaccctacc	tcacctgctt	actgacattg	tcttagctga	tcacaagatc	attatcagcc	960
tccattattc	cttactgtat	ataaaaataca	gagttttata	tttccctttc	ttcgtttttc	1020
accataattca	aaacctaaat	ttgtttttgc	agatggaatg	caaagtaatc	aagtgttcgt	1080
gctttcacct	agaagggtgt	ggtcctgaag	gaaagaggtc	cctaaatata	ccccaccctg	1140
gggtgctcctc	cttccctggg	accctgacta	ccagaagtca	gggtgctagag	cagctggaga	1200
agtgcagcag	cctgtgcttc	cacagatggg	gggtgctgctg	caacaaggct	ttcaatgtgc	1260
ccatcttagg	gggagaagct	agatcctgtg	cagcagcctg	gtaagtccctg	aggaggttcc	1320
attgctcttc	ctgctgctgt	cctttgcttc	tcaacggggc	tcgctctaca	gtctagagca	1380
catgcagcta	acttgtgcct	ctgcttatgc	atgagggtta	aattaacaac	cataaccttc	1440
atttgaagtt	caaagggtga	ttcaggatcc	tcaaagcatt	ttaaccttgc	cgcttaaaac	1500
ccaattttacc	gtgaaatggg	aattttgctg	cattgtttaa	ctgtagtgga	aaccatgcta	1560
tagtaataaa	ggttatataa	gagagaaatt	gaaattaaat	gtgtttttta	atttcaaaaa	1620
aaaatcaatc	tttaggatga	cttaaaaatt	gatttgccat	gtaaaatgta	tctgcatttt	1680
ttacacaaaa	cttggtttta	gcataaaatt	ttaaaactgt	actacttgat	gtattatata	1740
ttttgaacca	tatgtattaa	accataaaca	gtataatgtt	gttataataa	aacaggcaat	1800
aaatttataa	ataaaagctg	aaaaaaaaaa	aaaaaaaaaa	aaaa		1844

<210> 89

<211> 523

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(523)

<223> n = A,T,C or G

<400> 89

tttttttttt	tttttttagt	caatccacat	ttattgatca	cttattatgt	accaggcact	60
gggataaaga	tgactgttag	tcactcacag	taaggaagaa	aactagcaaa	taagacgatt	120
acaatatgat	gtagaaaatg	ctaagccaga	gatatagaaa	ggtcctattg	ggtccttctg	180
tcacctgtgc	tttccacatc	cctacccttc	acaggccttc	cctccagctt	cctgcccccg	240
ctccccactg	cagatccccct	gggattttgc	ctagagctaa	acgagganat	gggccccctg	300
gccctggcat	gacttgaacc	caaccacaga	ctgggaaagg	gagcctttcg	anagtggatc	360
actttgatna	gaaaacacat	agggaattga	agagaaantc	cccaaattggc	caccctgtgt	420
ggtgctcaag	aaaagtttgc	agaatggata	aatgaaggat	caaggggaatt	aatanatgaa	480
taattgaatg	gtggctcaat	aagaatgact	ncnttgaatg	acc		523

<210> 90

<211> 604

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(604)

<223> n = A,T,C or G

<400> 90

ccagtgtggt	ggaatgcaaa	gattacccccg	gaagctttcg	agaagctggg	attccctgca	60
gcaaaggaaa	tagccaatat	gtgtcgtttc	tatgaaatga	agccagaccg	agatgtcaat	120
ctcacccacc	aactaaatcc	caaagtcaaa	agcttcagcc	agtttatctc	agagaaccag	180
gggagccttc	aagggcattg	agaaaatcag	ctgttcagat	aggcctctgc	accacacagc	240
ctctttcttc	tctgatcctt	ttcctcttta	cggcacaaca	ttcatgtttg	acagaacatg	300
ctggaatgca	attgtttgca	acaccgaagg	atttcctgcg	gtcgcctctt	cagtaggaag	360
cactgcattg	gtgataggac	acggtaattt	gattcacatt	taacttgcta	gttagtgata	420
aggggtggta	cacctgtttg	gtaaaatgag	aagcctcgga	aacttgggag	cttctctcct	480
accactaatg	gggagggcag	attattactg	ggatttctcc	tggggtgaat	taatttcaag	540
ccctaattgc	tgaattccc	ctnggcaggc	tccagttttc	tcaactgcat	tgcaaaattc	600
cccc						604

<210> 91

<211> 858

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(858)

<223> n = A,T,C or G

<400> 91

tttttttttt	ttttttttta	tgattattat	tttttttatt	gatctttaca	tcctcagtgt	60
tggcagagtt	tctgatgctt	aataaacatt	tgttctgatc	agataagtgg	aaaaaattgt	120
catttcctta	ttcaagccat	gcttttctgt	gatattctga	tcctagtgtga	acatacagaa	180

ataaatgtct	aaaacagcac	ctcgattctc	gtctataaca	ggactaagtt	cactgtgatc	240
ttaaataagc	ttggctaaaa	tgggacatga	gtggaggtag	tcacacttca	gcgaagaaag	300
agaatctcct	gtataatctc	accaggagat	tcaacgaatt	ccaccacact	ggactagtgg	360
atcccccg	ctgcaggaat	tcgatatcaa	gcttatcgat	accgtcgacc	tcgagggggg	420
gccccgtacc	caattcgccc	tatagtgagt	cgtattacgc	gcgctcactg	gccgtcgttt	480
tacaacgtcg	tgactgggaa	aaccctggcg	ttaccaact	taatcgctt	gcagcacatc	540
cccttttcgc	cagctggcgt	aatagcgaan	agcccgccacc	gatcgccctt	ncaacagttg	600
cgagcctga	atggcgaatg	ggacgcgccc	tgtagcggcg	cattaaagcg	cggcngggtg	660
tggnggntcc	cccacgtgac	cgntacactt	ggcagcgctt	tacgcgggtc	nttcgctttc	720
ttcccttcc	ttctcgaccc	gttcgcggcg	tttccccgnn	agctnttaat	cgggggnctc	780
cctttanggg	tncnaattaa	nggnttacng	gaccttngan	cccaaaaact	ttgattaggg	840
ggaagggtccc	cgaagggg					858

<210> 92
 <211> 585
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (585)
 <223> n = A,T,C or G

<400> 92	
gttgaatctc	ctggtgagat
tccactcatg	tcccatttta
tagacgagaa	tcgaggtgct
atatcacaga	aaagcatggc
gaacaaatgt	ttattaagca
aaaaaataat	aatcatnann
ccagcttttg	ttcccttttag
ctgtttcctg	tgtgaaattg
gcntnangtg	taaaagcctg
tgcgctccac	ttgcccgctt
tatacaggag	attctctttc
tttaagatca	cagtgaactt
tttatttctg	tatgttcaac
aaatgacaat	tttttccact
tgccaacact	gaggatgtaa
nngaaggggcg	gccgccaccg
ggcgcttaatc	atgggtcatag
cacaattccn	cncaacatac
ctnactcaca	ttaattgngt
ggaaacctgt	tcgnc
	60
	120
	180
	240
	300
	360
	420
	480
	540
	585

<210> 93
 <211> 567
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (567)
 <223> n = A,T,C or G

<400> 93	
cggcagtgtt	gctgtctgcg
agactgcggc	tggggtgggc
ttccctgtac	ccaccttccc
ccagtttcc	tgtgtgatac
attaaattgc	tantgtttct
ccnccgngga	aacnccccct
gttaancnt	gggccaaanc
cccccnnc	ttccaaacc
ngnaattnaa	ccnaaccccc
ggaatctggc	tgaactggct
accgggggct	gctgtgaagg
gtttgtanag	gaaccttgtg
ttgctttttt	tgggaaatan
nnnnnnnnnn	nnnnnnnggg
ggttaattng	cnncnttggc
gttnatcccc	tcccaaatc
ancccgggg	gttgcctaan
ccacnngccc	cnctttccca
	60
	120
	180
	240
	300
	360
	420
	480
	540

nttcggggaa aaccctntcc gtgccca

567

<210> 94
<211> 620
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(620)
<223> n = A,T,C or G

<400> 94
actagtcaaa aatgctaaaa taatttggga gaaaatattt tttaagtagt gttatagttt 60
catgtttatc ttttattatg ttttgtgaag ttgtgtcttt tcactaatta cctatactat 120
gccaatattt ccttatatct atccataaca ttatactac atttgtaana naatatgcac 180
gtgaaactta acactttata aggtaaaaat gaggtttcca anatttaata atctgatcaa 240
gttcttggtta tttccaaata gaatggactt ggtctgttaa gggctaagga gaagaggaag 300
ataagggttaa aagttgttaa tgaccaaaca ttctaaaaga aatgcaaaaa aaaagtttat 360
tttcaagcct tcgaactatt taaggaaagc aaaatcattt cctaaatgca tatcatttgt 420
gagaatttct cattaatatc ctgaatcatt catttcaacta aggctcatgt tnactccgat 480
atgtctctaa gaaagtacta tttcatgggc caaacctggg tgccatantt gggtaaaggc 540
tttcccttaa gtgtgaaant atttaaaatg aaattttcct ctttttaaaa attctttana 600
agggttaagg gtgttgggga 620

<210> 95
<211> 470
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(470)
<223> n = A,T,C or G

<400> 95
ctcgaccttc tctgcacagc ggatgaaccc tgagcagctg aagaccagaa aagccactat 60
nactttntgc ttaattcang agcttacang attcttcaaa gagtnggtcc agcatccttt 120
gaaacatgag ttcttaccag cagaagcaga cctttacccc accacctcag cttcaacagc 180
agcaggtgaa acaacccatc cagcctccac ctnaggaaat atttgttccc acaaccaagg 240
agccatgcca ctcaaagggt ccacaacctg naaacacaaa nattccagag ccaggctgta 300
ccaagggtccc tgagccaggg ctgtaccaan gtccctgagc caggttgtag caangtccct 360
gagccaggat gtaccaaggt ccctgancca ggttggtcaa ggtccctgag ccaggctaca 420
ccaagggcct gngccaggca gcatcaangt ccctgaccaa ggcttatcaa 470

<210> 96
<211> 660
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(660)
<223> n = A,T,C or G

<400> 96

tttttttttt	tttttttttt	ggaattaaaa	gcaatttaaat	gagggcagag	caggaaacat	60
gcattttcttt	tcatttogaat	cttcagatga	accctgagca	gccgaagacc	agaaaagcca	120
tgaagacttt	ctgcttaatt	caggggctta	caggattctt	cagagtgtgt	gtgaacaaaa	180
gctttatagt	acgtattttt	aggatacaaa	taagagagag	actatggctt	ggggtgagaa	240
tgtactgatt	acaaggtcta	cagacaatta	agacacagaa	acagatggga	agagggtgnc	300
cagcatctgg	nggttggtt	ctcaagggtt	tgtctgtgca	ccaaattact	tctgcttggg	360
cttctgctga	gctgggcctg	gagtgaccgt	tgaaggacat	ggctctggta	cctttgtgta	420
gcctgncaca	ggaacttttg	tgtatccttg	ctcaggaact	ttgatggcac	ctggctcagg	480
aaacttgatg	aagccttggt	caagggtgct	tgatgcttgc	tggtctcagg	accttgngn	540
ancctgggct	canggacctt	tgncncaacc	ttggcttcaa	gggaccttg	gnacatcctg	600
gcnnagggac	ccttggncc	aacctgggc	tnagggacc	ctttgntnc	nanccttggc	660

<210> 97

<211> 441

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(441)

<223> n = A,T,C or G

<400> 97

gggaccatac	anagtattcc	tctcttcaca	ccaggaccag	ccactgttgc	agcatgagtt	60
cccagcagca	gaagcagccc	tgcatccccc	cccctcagct	tcagcagcag	caggtgaaac	120
agccttgcca	gcctccacct	caggaacctt	gcaccccaa	aaccaaggag	ccctgccacc	180
ccaaggtgcc	tgagccctgc	caccccaaag	tgccctgagc	ctgccagccc	aagggtccag	240
agccatgcca	ccccaaagtg	cctgagccct	gcccttcaat	agtcactcca	gcaccagccc	300
agcagaanac	caagcagaag	taatgtgggc	cacagccatg	cccttgagga	gccggccacc	360
agatgctgaa	tcccctatcc	cattctgtgt	atgagtccca	tttgccttgc	aattagcatt	420
ctgtctcccc	caaaaaaaaa	a				441

<210> 98

<211> 600

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(600)

<223> n = A,T,C or G

<400> 98

gtattcctct	cttcacacca	ggaccagcca	ctgttgcagc	atgagttccc	agcagcagaa	60
gcagccctgc	atcccacccc	ctcagcttca	gcagcagcag	gtgaaacagc	cttgccagcc	120
tccacctcag	gaacctatga	tccccaaaac	caaggagccc	tgccacccca	aggtgcctga	180
gccctgccac	cccaaagtgc	ctgagccctg	ccagcccaag	gttccagagc	catgccaccc	240
caagggtgct	gagccctgcc	cttcaatagt	cactccagca	ccagcccagc	agaanaccaa	300
gcagaagtaa	tgtggtccac	agccatgccc	ttgaggagcc	ggccaccana	tgctgaatcc	360
cctatcccat	tctgtgtatg	agtcccattt	gccttgcaat	tagcattctg	tctcccccaa	420
aaaagaatgt	gctatgaagc	tttctttcct	acacactctg	agtctctgaa	tgaagctgaa	480
ggtcttaant	acaganctag	ttttcagctg	ctcagaattc	tctgaagaaa	agatttaaga	540
tgaaaggcaa	atgattcagc	tccttattac	cccattaaat	tcnctttcaa	ttccaaaaaa	600

<210> 99
 <211> 667
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(667)
 <223> n = A,T,C or G

```

<400> 99
actagtgact gagttcctgg caaagaaatt tgacctggac cagttgataa ctcatgtttt    60
accattttaa aaaatcagtg aaggatttga gctgctcaat tcaggacaaa gcattcgaac    120
ggtcctgacg ttttgagatc caaagtggca ggaggtctgt gttgtcatgg tgaactggag    180
tttctcttgt gagagttccc tcatctgaaa tcatgtatct gtctcacaaa tacaagcata    240
agtagaagat ttgttgaaga catagaaccc ttataaagaa ttattaacct ttataaacat    300
ttaaagtctt gtgagcacct gggaattagt ataataacaa tgttnatatt tttgatttac    360
atthttgtaag gctataattg tatcttttaa gaaaacatac cttggatttc tatgttgaaa    420
tggagatttt taagagtttt aaccagctgc tgcagatata ttactcaaaa cagatatagc    480
gtataaagat atagtaaatt catctcctag agtaatatc acttaacaca ttggaaacta    540
ttatttttta gatttgaata tnaatgttat tttttaaaca cttgttatga gttacttggg    600
attacatttt gaaatcagtt cattccatga tgcanattac tgggattaga ttaagaaaga    660
cggaataa
cggaataa    667
  
```

<210> 100
 <211> 583
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(583)
 <223> n = A,T,C or G

```

<400> 100
gttttgtttg taagatgatc acagtcatgt tacactgatc taaaggacat atatataacc    60
ctttaaaaaa aaaatcactg cctcattctt atttcaagat gaatttctat acagactaga    120
tgtttttctg aagatcaatt agacattttg aaaatgattt aaagtgtttt ccttaattgtt    180
ctctgaaaac aagtttcttt tgtagtttta accaaaaaag tgcccttttt gtcactggat    240
tctcctagca ttcattgattt ttttttcata caatgaaatt aaaattgcta aaatcatgga    300
ctggctttct gggttgattt caggtaagat gtgtttaagg ccagagcttt tctcagtatt    360
tgattttttt ccccaatatt tgatttttta aaaatataca catnggtgct gcatttatat    420
ctgctggttt aaaattctgt catatttcac ttctagcctt ttagttatgg caaatcatat    480
tttactttta cttaaagcat ttggtnattt ggantatctg gttctannct aaaaaaanta    540
attctatnaa ttgaantttt ggtactcnnc catatttgga tcc
attctatnaa    583
  
```

<210> 101
 <211> 592
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 101

gtggagacgt	acaaagagca	gccgctcaag	acacctggga	agaaaaagaa	aggcaagccc	60
gggaaacgca	aggagcagga	aaagaaaaaa	cggcgaactc	gctctgcctg	gtagactct	120
ggagtgactg	ggagtgggct	agaaggggac	cacctgtctg	acacctccac	aacgtcgctg	180
gagctcgatt	cacggaggca	ttgaaatfff	cagcaganac	cttccaagga	catattgcag	240
gattctgtaa	tagtgaacat	atggaaagta	ttagaaatat	ttattgtctg	taaatactgt	300
aaatgcattg	gaataaaaact	gtctccccc	ttgtctctatg	aaactgcaca	ttggtcattg	360
tgaatatfff	tttttttgcc	aaggctaate	caattattat	tatcacattt	accataattt	420
atfffgtcca	ttgatgtatt	tatfffgtaa	atgtatcttg	gtgctgctga	atfffctatat	480
ttfffgtaca	taatgcnfff	anatatacct	atcaagfff	ttgataaatg	acncaatgaa	540
gtgnncnann	ttggnggttg	aatffaata	atgcctaatt	ttattatccc	aa	592

<210> 102

<211> 587

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(587)

<223> n = A,T,C or G

<400> 102

cgctctaagc	acttagacta	catcaggga	gaacacagac	cacatccctg	tcctcatgcg	60
gcttatgttt	tctggaagaa	agtggagacc	nagtccttgg	ctttagggct	ccccggctgg	120
gggctgtgca	ntccgggtcag	ggcgggaagg	gaaatgcacc	gctgcatgtg	aacttacagc	180
ccaggcggat	gccccttccc	ttagcactac	ctggcctcct	gcacccctc	gcctcatggt	240
cctccacact	tcaanaaatg	aanaacccca	tgggcccagc	cccttgccct	ggggaaccaa	300
ggcagccttc	caaaactcag	gggctgaagc	anactattag	ggcaggggct	gactttgggt	360
gacactgccc	attccctctc	agggcagctc	angtcaccn	ggnetcttga	accagcctg	420
ttcctttgaa	aaagggcaaa	actgaaaagg	gcttttccta	naaaaagaaa	aaccagggaa	480
ctttgccagg	gcttcnntnt	taccaaactn	ncttctcnng	gatttttaat	tccccattng	540
gcctccactt	accnggggcn	atgccccaaa	attaanaatt	tcccatc		587

<210> 103

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 103

anaggactgg	ccctacntgc	tctctctcgt	cctacctatc	aatgcccaac	atggcagaac	60
ctgcanccct	tggnactgc	anatggaaac	ctctcagtg	cttgacatca	ccctaccnt	120
gcggtggtgc	tccaccacaa	ccactttgac	tctgtgtgcc	ctgnanggtg	gnntctcctg	180
actggcagga	tggaacttan	ccnacatata	cctctgttcc	ctctgctnag	anaaagaatt	240
cccttaacat	gatataatcc	accatgcaa	ntngctactg	gccagctac	catttaccat	300
ttgcctacag	aatttcattc	agtctacact	ttggcattct	ctctggcgat	agagtgtggc	360
tgggctgacc	gcaaaagggtg	ccttacacac	tggccccac	cctcaaccgt	tgacncatca	420
gangettgc	tctctctct	gattnncccc	catgttggat	atcagggtgc	tcnagggtat	480
ggaaaagaaa	caaaac					496

<210> 104
 <211> 575
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (575)
 <223> n = A,T,C or G

<400> 104
 gcacctgctc tcaatccnnc tctcaccatg atcctccgcc tgcanaaact cctctgccaa 60
 ctatggangt ggtttcnggg gtggctcttg ccaactggga agaagccgtg gtgtctctac 120
 ctgttcaact cngtttgtgt ctgggggatc aactnggggc tatggaagcg gctnaactgt 180
 tgttttgggtg gaagggtggt taattggctt tgggaagtng cttatngaag ttggcctnng 240
 gaagttgcta ttgaaagtng ccntggaagt ngntttgggtg ggggggttttg ctggtggcct 300
 ttgttnaatt tgggtgcttt gtnaatggcg gccccctcnc ctgggcaatg aaaaaaatca 360
 ccnatgcngn aaacctcnac nnaacagcct gggcttcctt cacctcgaaa aaagttgctc 420
 cccccccaaa aaaggncaan cccctcaann tggaangttg aaaaaatcct cgaatgggga 480
 nccnnaaac aaaaancccc ccntttcccn gnaanggggg aaataccncc cccccactta 540
 cnaaaaccct tntaaaaaac cccccgggaa aaaaa 575

<210> 105
 <211> 619
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (619)
 <223> n = A,T,C or G

<400> 105
 cactagtagg atagaaacac tgtgtcccgga gagtaaggag agaagctact attgattaga 60
 gcctaaccga ggtaactgc aagaagaggc gggatacttt cagctttcca tgtaactgta 120
 tgcataaagc caatgtagtc cagtttctaa gatcatgttc caagctaact gaatccact 180
 tcaatacaca ctcatgaact cctgatggaa caataacagg cccaagcctg tggatgatg 240
 tgcacacttg ctagactcan aaaaaatact actctcataa atgggtggga gtattttggg 300
 gacaacctac tttgcttggc tgagtgaagg aatgatattc atatattcat ttattccatg 360
 gacatttagt tagtgctttt tatataccag gcatgatgct gaggtagact cttgtgtata 420
 tttccaaatt tttgtacagt cgctgcacat atttgaaatc atatattaag acttccaaaa 480
 aatgaagtcc ctgggttttc atggcaactt gatcagtaaa ggattcncct ctgtttggtg 540
 cttaaaacat ctactatatn gttnanatga aattcctttt cccncctcc cgaaaaaana 600
 aagtggtggg gaaaaaaaa 619

<210> 106
 <211> 506
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (506)
 <223> n = A,T,C or G

```

<400> 106
cattggttct ttcatttgct ntggaagtgt nnatctctaa cagtggacaa agttcccngt      60
gccttaaact ctgtnacact tttgggaant gaaaanttng tantatgata ggttattctg      120
angtanagat gttctggata ccattanatn tgccccnngt gtcagaggct catatttgtt      180
tatgtaaatg gtatntcatt cgctactatn antcaattng aaatanggtc tttgggttat      240
gaatantnng cagcncanct nanangctgt ctgtngtatt cattgtgggc atagcacctc      300
acancattgt aacctcnatc nagtgagaca nactagnaana ttcctagtga tggctcanga      360
ttccaaatgg nctcatntcn aatgtttaaa agttanttaa gtgtaagaaa tacagactgg      420
atgttccacc aactagtacc tgtaatgacn ggcctgtccc aacacatctc ccttttccat      480
gactgtggta ncccgcacg gaaaaa                                506

```

<210> 107

<211> 452

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(452)

<223> n = A,T,C or G

```

<400> 107
gttgagtctg tactaaacag taagatatct caatgaacca taaattcaac tttgtaaaaa      60
tcttttgaag catagataat attgttttgt aaatgtttct tttgttttgt aaatgtttct      120
tttaaagacc ctctattctc ataaaactct gcatgtagag gcttgtttac ctttctctct      180
ctaagggtta caataggagt ggtgatttga aaaatataaa attatgagat tggttttcct      240
gtggcataaa ttgcatcact gtatcatttt cttttttaac cggtaagant ttcagtttgt      300
tggaagagta ctgtganaac ccagtttccc gtccatctcc cttagggact acccatagaa      360
catgaaaagg tccccacnga agcaagaaga taagtcttct atggctgctg gttgcttaaa      420
ccacttttaa accaaaaaat tccccttgga aa                                452

```

<210> 108

<211> 502

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(502)

<223> n = A,T,C or G

```

<400> 108
atcttcttcc cttaattagt tnttatttat ntattaaatt ttattgcatg tcttgcaaaa      60
caaaaagaga ttgtagattg gcttctggct ccccaaaagc ccataacaga aagtaaccaca      120
agaccncaac tgaagcttaa aaaatctatc acatgtataa tacctttnga agaacattaa      180
tanagcatat aaaactttta acatntgctt aatgttgtnc aattataaaa ntaatngaaa      240
aaaaatgtccc tttaacatnc aatatcccac atagtgttat ttnaggggat taccnngnaa      300
naaaaaaagg gtagaaggga tttaatgaaa actctgcttn ccatttctgt ttanaaacgt      360
ctccagaaca aaaacttntc aantctttca gctaaccgca tttgagctna ggccactcaa      420
aaactccatt agnccactt tctaanggtc tctanagctt actaancctt ttgaccctt      480
accctggnta ctctgcct ca                                502

```

<210> 109

<211> 1308

<212> DNA

<213> Homo sapien

<400> 109

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accgcgaggtc tcgctaaaaat catcatggat tcacttggcg ccgtcagcac tcgacttggg      60
tttgatcttt tcaaagagct gaagaaaaca aatgatggca acatcttctt ttcccctgtg      120
ggcatcttga ctgcaattgg catggtcctc ctggggaccc gaggagccac cgcttcccg      180
ttggaggagg tgtttcactc tgaaaaagag acgaagagct caagaataaa ggctgaagaa      240
aaagagggtga ttgagaacac agaagcagta catcaacaat tccaaaagtt tttgactgaa      300
ataagcaaac tcactaatga ttatgaactg aacataacca acaggctgtt tggagaaaaa      360
acatacctct tccttcaaaa atacttagat tatgttgaaa aatattatca tgcactctctg      420
gaacctgttg attttgtaaa tgcagccgat gaaagtcgaa agaagattaa ttcctgggtt      480
gaaagcaaaa caaatgaaaa aatcaaggac ttgttcccag atggctctat tagtagctct      540
accaagctgg tgctggtgaa catggtttat tttaaagggc aatgggacag ggagttaaag      600
aaagaaaata ctaaggaaga gaaattttgg atgaataaga gcacaagtaa atctgtacag      660
atgatgacac agagccattc ctttagcttc actttcctgg aggacttgca ggccaaaatt      720
ctagggattc catataaaaa caacgaccta agcatgtttg tgcttctgcc caacgacatc      780
gatggcctgg agaagataat agataaaata agtcctgaga aattggtaga gtggactagt      840
ccagggcata tggaagaaag aaaggtgaat ctgcacttgc cccggtttga ggtggaggac      900
agttacgac tagaggcggc cctggctgcc atggggatgg gcgatgcctt cagtgcacac      960
aaagccgact actcgggaat gtcgtcaggc tccgggttgt acgcccagaa gttcctgcac      1020
agttcctttg tggcagtaac tgaggaaggc accgaggctg cagctgccac tggcataggc      1080
tttactgtca catccgcccc aggtcatgaa aatgttcaact gcaatcatcc cttcctgttc      1140
ttcatcaggc acaatgaatc caacagcatc ctcttcttcg gcagattttc ttctccttaa      1200
gatgatcggt gccatggcat tgctgctttt agcaaaaaac aactaccagt gttactcata      1260
tgattatgaa aatcgtccat tcttttaaat ggtggctcac ttgcattt      1308

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<210> 110

<211> 391

<212> PRT

<213> Homo sapien

<400> 110

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Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
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Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
 20         25         30
Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
 35         40         45
Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
 50         55         60
Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
 65         70         75         80
Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
 85         90         95
Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
100        105        110
Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
115        120        125
His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
130        135        140
Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145        150        155        160
Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
165        170        175

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Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
 180 185 190
 Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
 195 200 205
 Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
 210 215 220
 Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
 225 230 235 240
 Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
 245 250 255
 Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
 260 265 270
 Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
 275 280 285
 Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
 290 295 300
 Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
 305 310 315 320
 Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
 325 330 335
 Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Thr Gly Ile Gly
 340 345 350
 Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
 355 360 365
 Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
 370 375 380
 Phe Gly Arg Phe Ser Ser Pro
 385 390

<210> 111
 <211> 1419
 <212> DNA
 <213> Homo sapien

<400> 111
 ggagaactat aaattaagga tcccagctac ttaattgact tatgcttcct agttcgttgc 60
 ccagccacca cgtctctccc aaaaaccgga ggtctcgcta aaatcatcat ggattcactt 120
 ggcgccgtca gcactcgact tgggtttgat cttttcaaag agctgaagaa aacaaatgat 180
 ggcaacatct tcttttcccc tgtgggcata ttgactgcaa ttggcatggg cctcctgggg 240
 acccgaggag ccaccgcttc ccagttggag gaggtgtttc actctgaaaa agagacgaag 300
 agctcaagaa taaaggctga agaaaaagag gtggttaagaa taaaggctga aggaaaagag 360
 attgagaaca cagaagcagt acatcaacaa ttccaaaagt ttttgactga aataagcaaa 420
 ctactaatg attatgaact gaacataacc aacaggctgt ttggagaaaa aacatacctc 480
 ttccttcaaa aatacttaga ttatgttgaa aaatattatc atgcatctct ggaacctgtt 540
 gattttgtaa atgcagccga tgaaagtcga aagaagatta attcctgggt tgaaagcaaa 600
 acaaatgaaa aaatcaagga ctgttccca gatggctcta ttagtagctc taccaagctg 660
 gtgctggtga acatggttta ttttaaaggg caatgggaca gggagttaa gaaagaaat 720
 actaaggaag agaaattttg gatgaataag agcacaagta aatctgtaca gatgatgaca 780
 cagagccatt cctttagctt cactttcctg gaggacttgc aggccaaaat tctagggatt 840
 ccataaaaa acaacgacct aagcatgttt gtgcttctgc ccaacgacat cgtatggcctg 900
 gagaagataa tagataaaat aagtcctgag aaattggtag agtggactag tccaggcat 960
 atggaagaaa gaaagggtgaa tctgcacttg ccccggtttg aggtggagga cagttacgat 1020
 ctagaggcgg tcctggctgc catggggatg ggcgatgcct tcagttagca caaagccgac 1080
 tactcggaag tgctgtagg ctccgggttg tacgcccaga agttcctgca cagttccttt 1140
 gtggcagtaa ctgaggaagg caccgaggct gcagctgcca ctggcatagg ctttactgtc 1200

acatccgccc caggtcatga aaatgttcac tgcaatcatc ccttcctggt cttcatcagg 1260
 cacaatgaat ccaacagcat cctcttcttc gccagatttt cttctcctta agatgatcgt 1320
 tgccatggca ttgctgcttt tagcaaaaaa caactaccag tggtactcat atgattatga 1380
 aaatcggtcca ttctttttaa tggtgggtca cttgcattt 1419

<210> 112
 <211> 400
 <212> PRT
 <213> Homo sapien

<400> 112
 Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
 1 5 10 15
 Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
 20 25 30
 Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
 35 40 45
 Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
 50 55 60
 Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Val Arg Ile Lys Ala
 65 70 75 80
 Glu Gly Lys Glu Ile Glu Asn Thr Glu Ala Val His Gln Gln Phe Gln
 85 90 95
 Lys Phe Leu Thr Glu Ile Ser Lys Leu Thr Asn Asp Tyr Glu Leu Asn
 100 105 110
 Ile Thr Asn Arg Leu Phe Gly Glu Lys Thr Tyr Leu Phe Leu Gln Lys
 115 120 125
 Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr His Ala Ser Leu Glu Pro Val
 130 135 140
 Asp Phe Val Asn Ala Ala Asp Glu Ser Arg Lys Lys Ile Asn Ser Trp
 145 150 155 160
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Lys

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155

160

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<211> 6921

<212> DNA

<213> Homo sapien

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<211> 946

<212> DNA

<213> Homo sapien

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<213> Homo sapien

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8948

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<210> 123

<211> 2294

<212> DNA

<213> Homo sapien

<400> 123

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<210> 124

<211> 956

<212> DNA

<213> Homo sapien

<400> 124

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<210> 125

<211> 486

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (486)

<223> n = A,T,C or G

<400> 125

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<210> 126

<211> 3552

<212> DNA

<213> Homo sapien

<400> 126

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<210> 127

<211> 754

<212> DNA

<213> Homo sapien

<400> 127

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<210> 128

<211> 374

<212> DNA

<213> Homo sapien

<400> 128

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<210> 129

<211> 546

<212> DNA

<213> Homo sapien

<400> 129

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<210> 130

<211> 5156

<212> DNA

<213> Homo sapien

<400> 130

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 <211> 671
 <212> DNA
 <213> Homo sapien

<400> 131

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<210> 132

<211> 590

<212> DNA

<213> Homo sapien

<400> 132

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<210> 133

<211> 581

<212> DNA

<213> Homo sapien

<400> 133

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<210> 134

<211> 4797

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 134

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<211> 2856

<212> DNA

<213> Homo sapien

<400> 135

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atatcagcct	gagtctcctg	tgcccacatc	ccaggcttca	ccctgaatgg	ttccatgcct	1980
gaggggtggag	actaagccct	gtcgagacac	ttgccttctt	cacccagcta	atctgtaggg	2040
ctggacctat	gtcctaagga	cacactaatc	gaactatgaa	ctacaaagct	tctatcccag	2100
gaggtggcta	tggccacccg	ttctgctggc	ctggatctcc	ccactctagg	ggtcaggctc	2160
cattaggatt	tgccccttcc	catctcttcc	tacccaacca	ctcaaattaa	tctttcttta	2220
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atcacatatt	tgatagttag	tgttcaaaaa	aacactagtt	ttgtgccagc	cgtgatgctc	2820
aggcttgaaa	tgcattatt	ttgaatgtga	agggaa			2856

<210> 136

<211> 356

<212> DNA

<213> Homo sapien

<400> 136

ggtggagcca	aatgaagaaa	atgaagatga	aagagacaga	cacctcagtt	tttctggatc	60
aggcattgat	gatgatgaag	attttatctc	cagcaccatt	tcaaccacac	cacgggcttt	120
tgaccacaca	aaacagaacc	aggactggac	tcagtggaac	ccaagccatt	caaatccgga	180
agtgtactt	cagacaacca	caaggatgac	tgatgtagac	agaaatggca	ccactgctta	240
tgaaggaaac	tggaaaccag	aagcacaccc	tcccctcatt	caccatgagc	atcatgagga	300
agaagagacc	ccacattcta	caagcacaat	ccaggcaact	cctagtagta	caacgg	356

<210> 137

<211> 356

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(356)

<223> n = A,T,C or G

<400> 137

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gtcactggct	gcccccgaa	cagggcgctg	ctccatggct	ctgcttgtgg	tagtctgtgg	120
ctatgtctcc	cagcaaggac	agaaactcag	aaaaatcaat	cttcttatcc	tcattcttgt	180
cctttttctc	aaagacatcg	gcgaggtaat	ttgtgccctt	tttacctcgg	cccgcgacca	240
cgctaaggcc	aaanttcag	acanayggcc	gggccggtnc	nataggggan	cccaacttgg	300
ggaccctaac	tctggcgcg	aaacacangg	gcataagctt	gnttcctgtg	gggaaa	356

<210> 138

<211> 353

<212> DNA

<213> Homo sapien

<400> 138

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aatagacact	tagatttctc	tcttgtggga	agaaaccacc	tgtccatcca	ctgactcttc	120
tacattgatg	tggaaattgc	tgctgctacc	accacctcct	gaagaggctt	ccctgatgcc	180
aatgccagcc	atcttggcat	cctggccctc	gagcaggctg	cggtaagtag	cgatctcctg	240
ctccagccgt	gtctttatgt	caagcagcat	cttgtactcc	tggttctgag	cctccatctc	300
gcacgagac	tcactcagac	ctcgscgsg	mssmcgctam	gccgaattcc	agc	353

<210> 139

<211> 371

<212> DNA

<213> Homo sapien

<400> 139

agcgtggctc	cgcccgaggt	ccatccgaag	caagattgca	gatggcagtg	tgaagagaga	60
agacatattc	tacacttcaa	agctttgggt	caattcccat	cgaccagagt	tggtccgacc	120
agccttgga	aggtcactga	aaaatcttca	attggattat	gttgacctct	accttattca	180
ttttccagtg	tctgtaaagc	caggtgagga	agtgatccca	aaagatgaaa	atggaaaaat	240
actatttgac	acagtggatc	tctgtgccac	gtgggaggcc	gtggagaagt	gtaaagatgc	300
aggattggac	ctgcccgggc	ggccgctcga	aagccgaatt	ccagcacact	ggcggccggt	360
actagtggat	c					371

<210> 140

<211> 370

<212> DNA

<213> Homo sapien

<400> 140

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tgggagccag	ggcagatggt	gcattccttt	gtgtccctgt	aaatgtggga	ctacaagaag	120
aggagctgcc	tgagtggtag	tttctcttcc	tggtaatcct	ctggcccagc	ctcatggcag	180
aatagaggta	tttttaggct	atttttgtaa	tatggcttct	ggtcaaaatc	cctgtgtagc	240
tgaattccca	agccctgcat	tgtacagccc	cccactcccc	tcaccaccta	ataaagggaat	300
agttaacact	caaaaaaaaa	aaaaaacctg	cccggggcgc	cgctcgaaag	ccgaattcca	360
gcacactggc						370

<210> 141

<211> 371

<212> DNA

<213> Homo sapien

<400> 141

tagcgtggtc	gcggccgagg	tcctctgtgc	tgctgtcac	agcccgatgg	taccagcgca	60
gggtgtaggc	agtgcaggag	ccctcatcca	gtggcaggga	acagggggtca	tcactatccc	120

aaggagcttc	agggtcctgg	tactcctcca	cagaatactc	ggagtattca	gagtactcat	180
catcctcagg	gggtacccgc	tcttcctcct	ctgcatgaga	gacgcggagc	acaggcacag	240
catggagctg	ggagccggca	gtgtctgcag	cataactagg	gaggggtcgt	gatccagatg	300
cgatgaactg	gccctggcag	gcacagtgtc	gactcatctc	ttggcgacct	gcccggggcg	360
ccgctcgaag	c					371

<210> 142

<211> 343

<212> DNA

<213> Homo sapien

<400> 142

gcgttttgag	gccaatggtg	taaaaggaaa	tatcttcaca	taaaaactag	atggaagcat	60
tgtcagaaac	ctctttgtga	tgtttgcttt	caactcacag	agttgaacat	tccttttcat	120
agagcagttt	tgaaacactc	ttttgtagaa	tttgcaagcg	gatgattgga	tcgctatgag	180
gtcttcattg	gaaacgggat	acctttacat	aaaaactaga	cagtagcatt	ctcagaaatt	240
tctttgggat	gtgggcattc	aaccacaga	ggagaacttc	atttgataga	gcagttttga	300
aacacccttt	ttgtagaatc	tacaggtgga	catttagagt	gct		343

<210> 143

<211> 354

<212> DNA

<213> Homo sapien

<400> 143

aggtctgatg	gcagaaaaac	tcagactgtc	tgcaacttta	cagatggtgc	attggttcag	60
catcaggagt	gggatgggaa	ggaaagcaca	ataacaagaa	aattgaaaga	tgggaaatta	120
gtggtggagt	gtgtcatgaa	caatgtcacc	tgtactcgga	tctatgaaaa	agtagaataa	180
aaattccatc	atcacttttg	acaggagtta	attaagagaa	tgaccaagct	cagttcaatg	240
agcaaacttc	catactgttt	ctttcttttt	tttttcatta	ctgtgttcaa	ttatctttat	300
cataaacatt	ttacatgcag	ctatttcaaa	gtgtgttgga	ttaattagga	tcac	354

<210> 144

<211> 353

<212> DNA

<213> Homo sapien

<400> 144

ggtcaaggac	ctgggggacc	cccagggtcca	gcagccacat	gattctgcag	cagacaggga	60
cctagagcac	atctggatct	cagccccacc	cctggcaacc	tgctgccta	gagaactccc	120
aagatgacag	actaagtagg	attctgccat	ttagaataat	tctggtatcc	tgggcgttgc	180
gttaagtgtc	ttaactttca	ttctgtctta	cgatagtctt	cagaggtggg	aacagatgaa	240
gaaaccatgc	cccagagaag	gttaagtgtc	ttcctcttta	tggagccagt	gttccaacct	300
aggtttgcct	gataccagac	ctgtggcccc	acctcccatg	caggtctctg	tgg	353

<210> 145

<211> 371

<212> DNA

<213> Homo sapien

<400> 145

caggtctgtc	ataaactggt	ctggagtttc	tgacgactcc	ttgttcacca	aatgcaccat	60
ttcctgagac	ttgctggcct	ctccgttgag	tccacttggc	tttctgtcct	ccacagctcc	120
attgccactg	ttgatcacta	gctttttctt	ctgcccacac	cttcttcgac	tgttgactgc	180
aatgcaaact	gcaagaatca	aagccaaggc	caagagggat	gccaagatga	tcagccattc	240

tggaatttgg ggtgtcctta taggaccaga ggttgtgttt gctccacett cttgactccc	300
atgtgagacc tcggccgcga ccacgctaag ccgaattcca gcacactggc ggcccgttac	360
tagtggatcc g	371

<210> 146

<211> 355

<212> DNA

<213> Homo sapien

<400> 146

ggctcctccgt cctcttccca gaggtgtcgg ggcttggccc cagcctccat cttcgtctct	60
caggatggcg agtagcagcg gctccaaggc tgaattcatt gtcggaggga aatataaact	120
ggtacggaag atcgggtctg gctccttcgg ggacatctat ttggcgatca acatcaccaa	180
cggcgaggaa gtggcagtga agctagaatc tcagaaggcc aggcattcccc agttgctgta	240
cgagagcaag ctctataaga ttcttcaagg tggggttggc atccccaca tacggtggta	300
tggtcaggaa aaagactaca atgtactagt catggatctt ctgggacctt gcctc	355

<210> 147

<211> 355

<212> DNA

<213> Homo sapien

<400> 147

ggtctgttac aaaatgaaga cagacaacac aacatttact ctgtggagat atcctactca	60
tactatgcac gtgctgtgat tttgaacata actcgtccca aaaacttgtc acgatcatcc	120
tgacttttta ggttggctga tccatcaatc ttgcactcaa ctgttacttc ttcccagtg	180
ttgttaggag caaagctgac ctgaacagca accaatggct gtagataccc aacatgcagt	240
tttttcccat aatatgggaa atattttaag tctatcattc cattatgagg ataaactgct	300
acatttggtat tatcttcatt ctttgaacaa caatctatcc ttggcactcc ttcag	355

<210> 148

<211> 369

<212> DNA

<213> Homo sapien

<400> 148

aggtctctct cccctctccc ctctcctgcc agccaagtga agacatgett acttccccct	60
caccttcctt catgatgtgg gaagagtget gcaaccacgc cctagccaac accgcatgag	120
agggagtgtg ccgagggtct ctgagaaggt ttctctcaca tctagaaaga agcgcttaag	180
atgtggcagc cctcttctct caagtggctc ttgtcctggt gccctgggag ttctcaaatt	240
gctgcagcag cctccatcca gcctgaggat gacatcaata cacagaggaa gaagagtcag	300
gaaaagatga gagaagttac agactctcct gggcgacccc gagagcttac cattcctcag	360
acttcttca	369

<210> 149

<211> 620

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(620)

<223> n = A,T,C or G

<400> 149

actagtcaaa	aatgctaaaa	taatttgga	gaaaatattt	tttaagtagt	gttatagttt	60
catgtttatc	ttttattatg	ttttgtgaag	ttgtgtcttt	tcaactaatta	cctatactat	120
gccaatattt	ccttatatct	atccataaca	tttatactac	atgtgtaana	naatatgcac	180
gtgaaactta	acactttata	aggtaaaaat	gagggttcca	anatttaata	atctgatcaa	240
gttcttgtaa	tttccaaata	gaatggactt	ggctctgttaa	gggctaagga	gaagaggaag	300
ataagggttaa	aagtgtgtaa	tgaccaaaca	ttctaaaaga	aatgcaaaaa	aaaagtttat	360
tttcaagcct	tcgaactatt	taaggaaaagc	aaaatcattt	cctaaatgca	tatcatttgt	420
gagaatttct	cattaatatc	ctgaatcatt	catttcacta	aggctcatgt	tnactccgat	480
atgtctctaa	gaaagtacta	tttcatggtc	caaacctggc	tgccatantt	gggttaaaggc	540
tttcccttaa	gtgtgaaant	atttaaaatg	aaattttcct	ctttttaaaa	attctttana	600
aggggttaagg	gtgttgggga					620

<210> 150

<211> 371

<212> DNA

<213> Homo sapien

<400> 150

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gagcaaccag	tatcacttcc	ctgtttataa	aacctctaac	catctctttg	ttctttgaac	120
atgtgaaaa	ccacctgggc	tgcatgtatg	ccgaatttg	yaattctttt	ctctcaaagt	180
aaaatttaat	tttagggatt	catttctata	ttttcacata	tgtagtatta	ttatttcctt	240
atatgtgtaa	gggtgaaattt	atgggtattg	agtgtgcaag	aaaatatatt	tttaaagctt	300
tcatttttcc	cccagtgaat	gatttagaat	tttttatgta	aataacaga	atgttttttc	360
ttacttttat	a					371

<210> 151

<211> 4655

<212> DNA

<213> Homo sapien

<400> 151

gggacttgag	ttctgttatc	ttcttaagta	gattcatatt	gtaagggctc	cggggtgagg	60
gggttgga	aatcctggag	ccagaagaaa	ggacagcagc	attgatcaat	cttacagcta	120
acatgttgta	cctggaaaac	aatgcccaga	ctcaatttag	tgagccacag	tacacgaacc	180
tggggctcct	gaacagcatg	gaccagcaga	ttcagaacgg	ctcctcgccc	accagtcctt	240
ataacacaga	ccacgcgcag	aacagcgtca	cggcgccctc	gccctacgca	cagccagcgt	300
ccaccttcga	tgctctctct	ccatcacccg	ccatccctc	caacaccgac	taccagggcc	360
cgcacagttt	cgacgtgtcc	ttccagcagt	cgagcacgcg	caagtcggcc	acctggacgt	420
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acgagggaca	gattgcccc	yttagtcatt	tgattcgagt	agaggggaac	agccatgccc	660
agtatgtaga	agatcccatc	acaggaagac	agagtgtgct	ggtaccttat	gagccacccc	720
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cggatgaaga	tagcatcaga	aagcagcaag	tttcggacag	tacaaagaac	ggtgatggta	960
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tggtgaagat	caaagagtcc	ctggaactca	tgcagtacct	tcttcagcac	acaattgaaa	1140
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gagacatgaa	tggactcagc	cccacccagg	cactccctcc	cccactctcc	atgccatcca	1440
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ataaacagaa	atggaaagca	gagttttcat	taaatccctt	tacctttttt	ttttcttggt	4380
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tttttataat	tgtacaaaat	taagcaaatg	ttaaaagtgt	tatatgcttt	attaatgttt	4500
tcaaaaggta	ttatacatgt	gatacatttt	ttaagcttca	gttgcttgct	ttctgggtact	4560
ttctgttatg	ggcttttggtg	gagccagaag	ccaactacac	atctcttttt	gtttgccagg	4620
acatgcaata	aaatttataa	aataaataaa	aacta			4655

<210> 152
 <211> 586
 <212> PRT
 <213> Homo sapien

<400> 152
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 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Ser Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Val Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Val Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Leu Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380

Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
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<210> 153

<211> 2007

<212> DNA

<213> Homo sapien

<400> 153

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 tggccagggc aattttggag agcaaaaaat ttgcagttag agcagtgacc agggatgtga 180
 cttgacaaa tgccctggag ctccagcgcc ttggagctga ggtgggtcaaa ggtgacctga 240
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<210> 154

<211> 2148

<212> DNA

<213> Homo sapien

<400> 154

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tttcttcctt	actgtgagtg	actaacagtc	atctttatcc	cagtgcctgg	tacataataa	2100
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<210> 155
 <211> 153
 <212> PRT
 <213> Homo sapien

<400> 155
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 Pro Met Gly Asp Val Pro Met Asp Gly Ile Ser Val Ala Asp Ile Gly
 35 40 45
 Ala Ala Val Ser Ser Ile Phe Asn Ser Pro Glu Glu Phe Leu Gly Lys
 50 55 60
 Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65 70 75 80
 Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Ile Thr
 85 90 95
 Pro Glu Ala Phe Glu Lys Leu Gly Phe Pro Ala Ala Lys Glu Ile Ala
 100 105 110
 Asn Met Cys Arg Phe Tyr Glu Met Lys Pro Asp Arg Asp Val Asn Leu
 115 120 125
 Thr His Gln Leu Asn Pro Lys Val Lys Ser Phe Ser Gln Phe Ile Ser
 130 135 140
 Glu Asn Gln Gly Ala Phe Lys Gly Met
 145 150

<210> 156
 <211> 128
 <212> PRT
 <213> Homo sapien

<400> 156
 Met Thr Ser Val Arg Val Ala Ala Tyr Phe Glu Asn Phe Leu Ala Ala
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 Trp Arg Pro Val Lys Ala Ser Asp Gly Asp Tyr Tyr Thr Leu Ala Val
 20 25 30
 Pro Met Gly Asp Val Pro Met Asp Gly Ile Ser Val Ala Asp Ile Gly
 35 40 45
 Ala Ala Val Ser Ser Ile Phe Asn Ser Pro Glu Glu Phe Leu Gly Lys
 50 55 60
 Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65 70 75 80
 Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Thr Ile
 85 90 95
 Cys Ala Ile Asp Asp Gln Lys Thr Val Glu Glu Gly Phe Met Glu Asp
 100 105 110
 Val Gly Leu Ser Trp Ser Leu Arg Glu His Asp His Val Ala Gly Ala
 115 120 125

<210> 157
 <211> 424
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(424)
 <223> n = A,T,C or G

<400> 157

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aattcagtc	ccactgttat	attaccttct	ccaggaaccc	tccagtgggg	aaggctgcga	180
tattagattt	ccttgtatgc	aaagtttttg	ttgaaagctg	tgctcagagg	aggtgagagg	240
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tgct						424

<210> 158

<211> 2099

<212> DNA

<213> Homo sapien

<400> 158

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caaacggggc	tgacctccct	tcctggggag	caggaagggt	caggaagga	aaagaagtac	300
agaagatctg	gctaacaat	ttctgtatgg	cgaaagaaaa	attctaactt	gtacgcccctc	360
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gcagtcgttg	gaaacaggac	tcagggataa	accagcgcaa	tggtattggg	gacgtgcac	600
actttcatcg	ggggtgtcaa	caaacactcc	accagcatcg	ggaagggtgtg	gatcacagtc	660
atctttat	tcagagtc	gatcctcgtg	gtggctgccc	aggaagtgtg	gggtgacgag	720
caagaggact	tcgtctgcaa	cacactgcaa	ccgggatgca	aaaatgtgtg	ctatgaccac	780
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gcgtgctgg	tgcccatgca	tgtggcctac	tacaggcacg	aaaccactcg	caagttcagg	900
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gggtctatct	tgtaaatatt	gttttgcat	gtctgttggc	aaatttgtga	actgtcatga	1920
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cggaacagtg tggaagcaga aggttttttt aactcatccg tttgccaatc attgcaaaca 2040
actgaaatgt ggatgtgatt gcctcaataa agctcgtccc cattgcttaa aaaaaaaaaa 2099

<210> 159
<211> 291
<212> PRT
<213> Homo sapien

<400> 159
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Val Met Ile Leu Val Val Ala Ala Gln Glu Val Trp Gly Asp Glu Gln
35 40 45
Glu Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys
50 55 60
Tyr Asp His Phe Phe Pro Val Ser His Ile Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Phe Val Ser Thr Pro Ala Leu Leu Val Ala Met His Val Ala
85 90 95
Tyr Tyr Arg His Glu Thr Thr Arg Lys Phe Arg Arg Gly Glu Lys Arg
100 105 110
Asn Asp Phe Lys Asp Ile Glu Asp Ile Lys Lys Gln Lys Val Arg Ile
115 120 125
Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Ile
130 135 140
Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Phe Leu Tyr Asn Gly
145 150 155 160
Tyr His Leu Pro Trp Val Leu Lys Cys Gly Ile Asp Pro Cys Pro Asn
165 170 175
Leu Val Asp Cys Phe Ile Ser Arg Pro Thr Glu Lys Thr Val Phe Thr
180 185 190
Ile Phe Met Ile Ser Ala Ser Val Ile Cys Met Leu Leu Asn Val Ala
195 200 205
Glu Leu Cys Tyr Leu Leu Leu Lys Val Cys Phe Arg Arg Ser Lys Arg
210 215 220
Ala Gln Thr Gln Lys Asn His Pro Asn His Ala Leu Lys Glu Ser Lys
225 230 235 240
Gln Asn Glu Met Asn Glu Leu Ile Ser Asp Ser Gly Gln Asn Ala Ile
245 250 255
Thr Gly Ser Gln Ala Lys His Phe Lys Val Lys Cys Ser Cys Val Ile
260 265 270
Arg Arg Leu Leu Ser Ser Pro Glu Gly Asn Thr Asn Leu Lys Val Pro
275 280 285
Ser Val Ala
290

<210> 160
<211> 3951
<212> DNA
<213> Homo sapien

<400> 160
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gaacctcatc	tcaaacatta	aggaaatgat	aactgaagct	tcattttacc	tatttaatgc	300
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taataataac	agcaaaaata	aacaagaatc	atatgaaaag	gcaaatgtca	tagtgactga	420
ctggtatggg	gcacatggag	atgatccata	caccctacaa	tacagagggg	gtggaaaaga	480
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tgagtataac	aatgacaaac	ctttctacat	aaatgggcaa	aatcaaatta	aagtgacaag	660
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ctgtattatt	agtaagcttt	ttaaagaagg	atgcaccttt	atctacaata	gcacccaaaa	780
tgcaactgca	tcaataatgt	tcatgcaaag	tttatcttct	gtgggtgaat	tttgtaatgc	840
aagtaccac	aaccaagaag	caccaaacct	acagaaccag	atgtgcagcc	tcagaagtgc	900
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<210> 161

<211> 943

<212> PRT

<213> Homo sapien

<400> 161

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Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
35 40 45
Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
50 55 60
Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
65 70 75 80
Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn
85 90 95
Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile
100 105 110
Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln
115 120 125
Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn
130 135 140
Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg
145 150 155 160
Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu
165 170 175
Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys
180 185 190
Val Thr Arg Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys
195 200 205
Gly Pro Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu
210 215 220
Gly Cys Thr Phe Ile Tyr Asn Ser Thr Gln Asn Ala Thr Ala Ser Ile
225 230 235 240
Met Phe Met Gln Ser Leu Ser Ser Val Val Glu Phe Cys Asn Ala Ser
245 250 255
Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser Leu
260 265 270
Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His His Ser
275 280 285
Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu
290 295 300

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Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu Asp Val Ser Ser
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 Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu Gln Gln Ala Ala Glu
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 Phe Tyr Leu Met Gln Ile Val Glu Ile His Thr Phe Val Gly Ile Ala
 340 345 350
 Ser Phe Asp Ser Lys Gly Glu Ile Arg Ala Gln Leu His Gln Ile Asn
 355 360 365
 Ser Asn Asp Asp Arg Lys Leu Leu Val Ser Tyr Leu Pro Thr Thr Val
 370 375 380
 Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe
 385 390 395 400
 Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile
 405 410 415
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 420 425 430
 Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
 435 440 445
 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
 450 455 460
 Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe
 465 470 475 480
 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
 485 490 495
 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
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 Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp
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 Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
 565 570 575
 Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr
 580 585 590
 Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu
 595 600 605
 Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile
 610 615 620
 Tyr Ala Asn Val Lys Gln Gly Phe Tyr Pro Ile Leu Asn Ala Thr Val
 625 630 635 640
 Thr Ala Thr Val Glu Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu
 645 650 655
 Leu Asp Asp Gly Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr
 660 665 670
 Ser Arg Tyr Phe Phe Ser Phe Ala Ala Asn Gly Arg Tyr Ser Leu Lys
 675 680 685
 Val His Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile
 690 695 700
 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn
 705 710 715 720
 Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu
 725 730 735
 Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val

	740		745		750
Leu Gly Val	Pro Ala Gly	Pro His	Pro Asp Val	Phe Pro	Pro Cys Lys
755		760		765	
Ile Ile Asp	Leu Glu Ala	Val Lys	Val Glu Glu	Glu Leu Thr	Leu Ser
770		775		780	
Trp Thr Ala	Pro Gly Glu	Asp Phe	Asp Gln Gly	Gln Ala Thr	Ser Tyr
785		790		795	800
Glu Ile Arg	Met Ser Lys	Ser Leu	Gln Asn Ile	Gln Asp Asp	Phe Asn
	805		810		815
Asn Ala Ile	Leu Val Asn	Thr Ser	Lys Arg Asn	Pro Gln Gln	Ala Gly
	820		825		830
Ile Arg Glu	Ile Phe Thr	Phe Ser	Pro Gln Ile	Ser Thr Asn	Gly Pro
	835		840		845
Glu His Gln	Pro Asn Gly	Glu Thr	His Glu Ser	His Arg Ile	Tyr Val
	850		855		860
Ala Ile Arg	Ala Met Asp	Arg Asn	Ser Leu Gln	Ser Ala Val	Ser Asn
865		870		875	880
Ile Ala Gln	Ala Pro Leu	Phe Ile	Pro Pro Asn	Ser Asp Pro	Val Pro
	885		890		895
Ala Arg Asp	Tyr Leu Ile	Leu Lys	Gly Val Leu	Thr Ala Met	Gly Leu
	900		905		910
Ile Gly Ile	Ile Cys Leu	Ile Ile	Val Val Thr	His His Thr	Leu Ser
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Arg Lys Lys	Arg Ala Asp	Lys Lys	Glu Asn Gly	Thr Lys Leu	Leu
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<210> 162
 <211> 498
 <212> DNA
 <213> Homo sapien

<400> 162

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<210> 163
 <211> 1128
 <212> DNA
 <213> Homo sapien

<400> 163

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<210> 164
 <211> 1310
 <212> DNA
 <213> Homo sapien

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<400> 164
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<210> 165
 <211> 177
 <212> PRT
 <213> Homo sapien

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<400> 165
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Arg Leu Lys Arg Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly
          35          40          45
Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile

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50 55 60
 Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr Ser Glu Val Ser Pro
 65 70 75 80
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly
 85 90 95
 Ser Asp Asp Glu Gly Arg Tyr Leu Thr Gln Glu Thr Asn Lys Val Glu
 100 105 110
 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Lys Gly
 115 120 125
 Lys Pro Gly Lys Arg Lys Glu Gln Glu Lys Lys Lys Arg Arg Thr Arg
 130 135 140
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 145 150 155 160
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 165 170 175
 His

<210> 166
 <211> 177
 <212> PRT
 <213> Homo sapien

<400> 166
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 35 40 45
 Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile
 50 55 60
 Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr Ser Glu Val Ser Pro
 65 70 75 80
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly
 85 90 95
 Ser Asp Asp Glu Gly Arg Tyr Leu Thr Gln Glu Thr Asn Lys Val Glu
 100 105 110
 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Lys Gly
 115 120 125
 Lys Pro Gly Lys Arg Lys Glu Gln Glu Lys Lys Lys Arg Arg Thr Arg
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 165 170 175
 His

<210> 167
 <211> 3362
 <212> DNA
 <213> Homo sapien

<400> 167

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 tt 3362

<210> 168
 <211> 2784
 <212> DNA
 <213> Homo sapien

<400> 168

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2784

<210> 169

<211> 592

<212> PRT

<213> Homo sapien

<400> 169

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			20					25					30		
Val	Gln	Leu	Gln	Asp	Asn	Gly	Tyr	Asn	Gly	Leu	Leu	Ile	Ala	Ile	Asn
			35				40						45		
Pro	Gln	Val	Pro	Glu	Asn	Gln	Asn	Leu	Ile	Ser	Asn	Ile	Lys	Glu	Met
			50			55					60				
Ile	Thr	Glu	Ala	Ser	Phe	Tyr	Leu	Phe	Asn	Ala	Thr	Lys	Arg	Arg	Val
65					70				75					80	
Phe	Phe	Arg	Asn	Ile	Lys	Ile	Leu	Ile	Pro	Ala	Thr	Trp	Lys	Ala	Asn
				85					90					95	
Asn	Asn	Ser	Lys	Ile	Lys	Gln	Glu	Ser	Tyr	Glu	Lys	Ala	Asn	Val	Ile
			100					105					110		
Val	Thr	Asp	Trp	Tyr	Gly	Ala	His	Gly	Asp	Asp	Pro	Tyr	Thr	Leu	Gln
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Tyr	Arg	Gly	Cys	Gly	Lys	Glu	Gly	Lys	Tyr	Ile	His	Phe	Thr	Pro	Asn
		130				135					140				
Phe	Leu	Leu	Asn	Asp	Asn	Leu	Thr	Ala	Gly	Tyr	Gly	Ser	Arg	Gly	Arg
145					150				155					160	
Val	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	Asp	Glu
				165					170					175	
Tyr	Asn	Asn	Asp	Lys	Pro	Phe	Tyr	Ile	Asn	Gly	Gln	Asn	Gln	Ile	Lys
			180					185					190		
Val	Thr	Arg	Cys	Ser	Ser	Asp	Ile	Thr	Gly	Ile	Phe	Val	Cys	Glu	Lys
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Gly	Pro	Cys	Pro	Gln	Glu	Asn	Cys	Ile	Ile	Ser	Lys	Leu	Phe	Lys	Glu
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Gly	Cys	Thr	Phe	Ile	Tyr	Asn	Ser	Thr	Gln	Asn	Ala	Thr	Ala	Ser	Ile
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Met	Phe	Met	Gln	Ser	Leu	Ser	Ser	Val	Val	Glu	Phe	Cys	Asn	Ala	Ser
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Thr	His	Asn	Gln	Glu	Ala	Pro	Asn	Leu	Gln	Asn	Gln	Met	Cys	Ser	Leu
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Arg	Ser	Ala	Trp	Asp	Val	Ile	Thr	Asp	Ser	Ala	Asp	Phe	His	His	Ser
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Phe	Pro	Met	Asn	Gly	Thr	Glu	Leu	Pro	Pro	Pro	Pro	Thr	Phe	Ser	Leu
		290				295					300				
Val	Glu	Ala	Gly	Asp	Lys	Val	Val	Cys	Leu	Val	Leu	Asp	Val	Ser	Ser
305					310					315				320	
Lys	Met	Ala	Glu	Ala	Asp	Arg	Leu	Leu	Gln	Leu	Gln	Gln	Ala	Ala	Glu
				325					330					335	
Phe	Tyr	Leu	Met	Gln	Ile	Val	Glu	Ile	His	Thr	Phe	Val	Gly	Ile	Ala
			340					345					350		
Ser	Phe	Asp	Ser	Lys	Gly	Glu	Ile	Arg	Ala	Gln	Leu	His	Gln	Ile	Asn
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Ser	Asn	Asp	Asp	Arg	Lys	Leu	Leu	Val	Ser	Tyr	Leu	Pro	Thr	Thr	Val

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Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe
385              390              395              400
Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile
      405              410              415
Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr
      420              425              430
Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
      435              440              445
Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
      450              455              460
Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe
465              470              475              480
Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
      485              490              495
Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
      500              505              510
Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val
      515              520              525
Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp
      530              535              540
Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg
545              550              555              560
Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
      565              570              575
Tyr Thr Leu Met Cys Phe His His Ala Lys Leu Leu Thr Trp Lys Leu
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<210> 170
 <211> 791
 <212> PRT
 <213> Homo sapien

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Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
      20              25              30
Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
      35              40              45
Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
      50              55              60
Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
65              70              75              80
Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn
      85              90              95
Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile
      100             105             110
Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln
      115             120             125
Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn
      130             135             140
Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg
145             150             155             160
Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu

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Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile
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 Tyr Ala Asn Val Lys Gln Gly Phe Tyr Pro Ile Leu Asn Ala Thr Val
 625 630 635 640
 Thr Ala Thr Val Glu Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu
 645 650 655
 Leu Asp Asp Gly Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr
 660 665 670
 Ser Arg Tyr Phe Phe Ser Phe Ala Ala Asn Gly Arg Tyr Ser Leu Lys
 675 680 685
 Val His Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile
 690 695 700
 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn
 705 710 715 720
 Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu
 725 730 735
 Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val
 740 745 750
 Leu Gly Val Pro Ala Gly Pro His Pro Asp Val Phe Pro Pro Cys Lys
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 Asp Ser Thr Trp Arg Arg Leu
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<210> 171
 <211> 1491
 <212> DNA
 <213> Homo sapien

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1491

<210> 172
 <211> 364
 <212> PRT
 <213> Homo sapien

<400> 172
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 35 40 45
 Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His
 50 55 60
 Gly Ala Asn Arg Phe Val Pro Lys Ser Lys Ala Leu Glu Ala Val Lys
 65 70 75 80
 Leu Ala Ile Glu Ala Gly Phe His His Ile Asp Ser Ala His Val Tyr
 85 90 95
 Asn Asn Glu Glu Gln Val Gly Leu Ala Ile Arg Ser Lys Ile Ala Asp
 100 105 110
 Gly Ser Val Lys Arg Glu Asp Ile Phe Tyr Thr Ser Lys Leu Trp Ser
 115 120 125
 Asn Ser His Arg Pro Glu Leu Val Arg Pro Ala Leu Glu Arg Ser Leu
 130 135 140
 Lys Asn Leu Gln Leu Asp Tyr Val Asp Leu Tyr Leu Ile His Phe Pro
 145 150 155 160
 Val Ser Val Lys Pro Gly Glu Glu Val Ile Pro Lys Asp Glu Asn Gly
 165 170 175
 Lys Ile Leu Phe Asp Thr Val Asp Leu Cys Ala Thr Trp Glu Ala Met
 180 185 190
 Glu Lys Cys Lys Asp Ala Gly Leu Ala Lys Ser Ile Gly Val Ser Asn
 195 200 205
 Phe Asn His Arg Leu Leu Glu Met Ile Leu Asn Lys Pro Gly Leu Lys
 210 215 220
 Tyr Lys Pro Val Cys Asn Gln Val Glu Cys His Pro Tyr Phe Asn Gln
 225 230 235 240
 Arg Lys Leu Leu Asp Phe Cys Lys Ser Lys Asp Ile Val Leu Val Ala
 245 250 255
 Tyr Ser Ala Leu Gly Ser His Arg Glu Glu Pro Trp Val Asp Pro Asn
 260 265 270
 Ser Pro Val Leu Leu Glu Asp Pro Val Leu Cys Ala Leu Ala Lys Lys
 275 280 285
 His Lys Arg Thr Pro Ala Leu Ile Ala Leu Arg Tyr Gln Leu Gln Arg
 290 295 300
 Gly Val Val Val Leu Ala Lys Ser Tyr Asn Glu Gln Arg Ile Arg Gln
 305 310 315 320
 Asn Val Gln Val Phe Glu Phe Gln Leu Thr Ser Glu Glu Met Lys Ala
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<210> 174
<211> 238
<212> PRT
<213> Homo sapiens
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Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu		
50	55	60
Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp		
65	70	75 80
Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp Trp Lys Cys		
	85	90 95
Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly Cys Gln Ser		
	100	105 110
Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Met Leu Phe Cys		
	115	120 125
Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu		
	130	135 140
Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu		
	145	150 155 160
Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val		
	165	170 175
Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala Val Thr Tyr		
	180	185 190
Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu		
	195	200 205
Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp		
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Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala		
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<210> 175

<211> 4181

<212> DNA

<213> Homo sapiens

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gcaaaattgt	tccttttttt	tgaaaatttt	atatacttta	taatgataga	agtccaaccg	2640
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acacagttat	tagttaaatc	aaatgttcaa	aaatacggag	cagtgcctag	tatctggaga	2820
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gagcttttct	cagtatttga	tttttttccc	caatatttga	ttttttaaaa	atatacacat	3900
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gctaagaaat	aattcnataa	ttgagttttg	tactcnccaa	anatgggtca	ttcctcatgn	4080
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4181

<210> 176

<211> 580

<212> PRT

<213> Homo sapiens

<400> 176

Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
5 10 15

Asp Leu -Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100 105 110

Val	Asn	Thr	Asp	Ser	Glu	Thr	Ala	Val	Val	Asn	Val	Thr	Tyr	Ser	Ser
	115						120					125			

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
180 185 190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
195 200 205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
210 215 220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225 230 235 240

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
245 250 255

Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
 260 265 270
 Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
 275 280 285
 Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu Gln
 290 295 300
 Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu
 305 310 315 320
 Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys
 325 330 335
 Ala Lys Ala Glu Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu
 340 345 350
 Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu
 355 360 365
 Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro
 370 375 380
 Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe
 385 390 395 400
 Glu Gln Ser Glu Thr Glu Thr Val His Gln Phe Ile Pro Ala Leu Ser
 405 410 415
 Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser
 420 425 430
 Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp
 435 440 445
 Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
 450 455 460
 Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val
 465 470 475 480
 Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
 485 490 495
 Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
 500 505 510
 Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
 515 520 525
 Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
 530 535 540

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
 545 550 555 560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser
 565 570 575

Arg Arg Lys

<210> 177
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 177
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 agatccaaac aaatacacat tctgtgtttt agctcagtg tttctaaaaa aagaaactgc 120
 cacacagcaa aaaattgttt actttgttgg acaaaccaaa tcagttctca aaaaatgacc 180
 ggtgcttata aaaagttata aatatcgagt agctctaaaa caaacacact gaccaagagg 240
 gaagtgaagt tgtgcttagt atttacattg gatgccagtt ttgtaatcac tgacttatgt 300
 gcaaaactgg gcagaaattc tataaactct ttgctgtttt tgatacctgc tttttgtttc 360
 attttgtttt gttttgtaaa aatgataaaa ctccagaaaa t 401

<210> 178
 <211> 561
 <212> DNA
 <213> Homo sapiens

<400> 178
 acgcctttca aggggtgtacg caaagcactc attgataccc ttttggtatgg ctatgaaaca 60
 gcccgctatg ggacaggggt ctttggccag aatgagtacc tacgctatca ggaggccctg 120
 agtgagctgg ccaactgcgt taaagcacga attgggagct ctcagcgaca tcaccagtca 180
 gcagccaaag acctaactca gtcccctgag gtctcccaa caaccatcca ggtgacatac 240
 ctcccctcca gtcagaagag taaacgtgcc aagcacttcc ttgaattgaa gagctttaag 300
 gataactata acacattgga gagtactctg tgacggagct gaaggactct tgccgtagat 360
 taagccagtc agttgcaatg tgcaagacag gctgcttgcc gggccgccct cggaacatct 420
 ggcccagcag gccagactg tatccatcca agttcccgtt gtatccagag ttcttagagc 480
 ttgtgtctaa agggtaattc cccaaccctt ccttatgagc atttttagaa cattggctaa 540
 gactattttc cccagtagc g 561

<210> 179
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 179
 cccaacgcgt ttgcaaatat tcccctggta gectacttcc ttacccccga atattggtaa 60
 gatcgagcaa tggcttcagg acatgggttc tcttctctg tgatcattca agtgetcact 120
 gcatgaagac tggcttgtct cagtgtttca acctcaccag ggctgtctct tggccacac 180
 ctctctccct gttagtgcg tatgacagcc cccatcaaat gaccttgcc aagtcacggt 240
 ttctctgtgg tcaagggtgg ttggctgatt ggtggaaagt aggggtggacc aaaggaggcc 300
 acgtgagcag tcagcaccag ttctgcacca gcagcgcctc cgtcctagtg ggtgttcctg 360
 tttctctctg ccttgggtgg gctagggcct gatcgaggaa gatgccttg caggaggagg 420
 aggataagtg ggatctacca attgattctg gcaaaacaat ttctaagatt tttttgcttt 480

atgtgggaaa cagatctaaa tctcatttta tgctgtattt t 521

<210> 180

<211> 417

<212> DNA

<213> Homo sapiens

<400> 180

ggtggaattc gccgaagatg gcggaggtgc aggtcctggt gcttgatggt cgaggccatc 60
tcctgggccg cctggcgcc atcgtggcta aacaggtact gctgggccgg aaggtggtgg 120
tcgtacgtcg tgaaggcatc aacatttctg gcaatttcta cagaaacaag ttgaagtacc 180
tggttttct cgcgaagcgg atgaacacca acccttccc agggccctac cacttccggg 240
ccccagccg catcttctgg cggaccgtgc gaggtatgct gcccacaaa accaagcgag 300
gccaggccgc tctggaccgt ctcaagggtg ttgacggcat cccaccgccc tacgacaaga 360
aaaagcggat ggtggttcct gctgcctca aggtcgtgcg tctgaagcct acaagaa 417

<210> 181

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (35)

<223> n=A,T,C or G

<400> 181

gatttcttct aaataggatg taaaacttct ttcanattac tcttcctcag tcctgcctgc 60
caagaactca agtgtaactg tgataaaata acctttccca ggtatattgg caggtatgtg 120
tgtaatctca gaatacacag gtgacataga tatgatatga caactggtaa tgggtggattc 180
atttacattg tttacacttc tatgaccagg ccttaaggga aggtcagttt tttaaaaaac 240
caagtagtgt cttcctacct atctccagat acatgtcaaa aaa 283

<210> 182

<211> 401

<212> DNA

<213> Homo sapiens

<400> 182

atattcttgc tgcttatgca gctgacattg ttgcctccc taaagcaacc aagtagcctt 60
tatttccac agtgaaagaa aacgctggcc tatcagttac attacaaaag gcagatttca 120
agaggattga gtaagtagtt ggatggcttt cataaaaaca agaattcaag aagaggattc 180
atgctttaag aaacatttgt tataattcc tcacaaatta tacctgggat aaaaactatg 240
tagcaggcag tgtgttttcc ttccatgtct ctctgcacta cctgcagtgt gtcctctgag 300
gctgcaagtc tgtcctatct gaattcccag cagaagcact aagaagctcc accctatcac 360
ctagcagata aaactatggg gaaaacttaa atctgtgcat a 401

<210> 183

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (325)

<223> n=A,T,C or G

<400> 183

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accatcatgc tttgatgttc cctgtgtctt ctctctcttg ctctcaagag caaagggttaa 120
tttaaggaca aagatgaagt cactgtaaac taatctgtca ttgtttttac ctctcttttc 180
tttttcagtg cagaaattaa aagtaagtat aaagcaccgt gattgggagt gtttttgctg 240
gtgtcggaat cactggtaaa tgttggtga gaacaatccc tccccttgca cttgtgaaaa 300
cactttgagc gctttaagag attancctga gaaataatta aatatctttt ctcttcaaaa 360
aaaaaa 366
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<210> 184

<211> 370

<212> DNA

<213> Homo sapiens

<400> 184

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tcttacttca aaagaaaaat aaacataaaa aataagttgc tggttcctaa caggaaaaat 60
tttaataatt gtactgagag aaactgctta cgtacacatt gcagatcaaa tatttgaggt 120
taaaatgtta gtctacatag atgggtgatt gtaactttat tgccattaaa agatttcaaa 180
ttgcattcat gcttctgtgt acacataatg aaaaatgggc aaataatgaa gatctctcct 240
tcagtctgct ctgtttaatt ctgctgtctg ctcttctcta atgctgcgtc cctaattgta 300
cacagtttag tgatatctag gagtataaag ttgtcgccca tcaataaaaa tcacaaagtt 360
ggtttaaaaa 370
```

<210> 185

<211> 107

<212> DNA

<213> Homo sapiens

<400> 185

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ctcatattat tttccttttg agaaattgga aactctttct gttgctatta tattaataaa 60
gttggtgttt atttctggt agtcaccttc cccatttaaa aaaaaaa 107
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<210> 186

<211> 309

<212> DNA

<213> Homo sapiens

<400> 186

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gaaaggatgg ctctgggtgc cacagagctg ggacttcatg ttcttctaga gagggccaca 60
agagggccac aggggtggcc gggagttgtc agctgatgcc tgctgagagg caggaattgt 120
gccagtgaat gacagtcagt agggagtgtc tcttcttggg gaggaagaa ggtagagcct 180
ttctgtctga atgaaaggcc aaggctacag tacagggccc cgccccagcc aggggtgtta 240
tgcccacgta gtggaggcct ctggcagatc ctgcattcca aggtcactgg actgtacgtt 300
tttatggtt 309
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<210> 187

<211> 477

<212> DNA

<213> Homo sapiens

<400> 187

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ttcagtccta gcaagaagcg agaattctga gatcctccag aaagtcgagc agcaccacc 60
tccaacctcg ggccagtgtc ttcaggcttt actggggacc tgcgagctgg cctaattgtg 120
```

```

tggcctgcaa gccaggccat cctctgggcgc cacagacgag ctccgagcca ggtcaggctt 180
cggaggccac aagctcagcc tcaggcccag gcactgattg tggcagaggg gccactaccc 240
aaggtctagc taggcccag acctagttac ccagacagtg agaagcccct ggaaggcaga 300
aaagttggga gcatggcaga cagggaaggg aaacattttc agggaaaaga catgtatcac 360
atgtcttcag aagcaagtca ggtttcatgt aaccgagtgt cctcttgctg gtccaaaagt 420
agcccagggc tgtagcacag gcttcacagt gattttgtgt tcagccgtga gtcacac 477

```

<210> 188

<211> 220

<212> DNA

<213> Homo sapiens

<400> 188

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taaatatggg agatattaat attcctctta gatgaccagt gattccaatt gtcccaagtt 60
ttaaataagt accctgtgag tatgagataa attagtgcac atcagaacaa gtttcagtat 120
cagatgttca agaggaagtt gctattgcat tgattttaat atttgtagat aaacactgat 180
ttttttgagc attattttgt atttgttgta ctttaatacc 220

```

<210> 189

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (76)

<223> n=A,T,C or G

<221> unsure

<222> (77)

<223> n=A,T,C or G

<400> 189

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accatcttga cagaggatac atgctcccaa aacgtttgtt accacactta aaaatcactg 60
ccatcattaa gcatcnnntt caaaattata gccattcatg atttactttt tccagatgac 120
tatcattatt ctagtccctt gaatttgtaa ggggaaaaaa aacaaaaaca aaaacttacg 180
atgcactttt ctccagcaca tcagatttca aattgaaaat taaagacatg ctatggtaat 240
gcacttgcta gtactacaca ctttgtacaa caaaaaacag aggcaagaaa caacggaaag 300
agaaaagcct tcctttgttg gcccttaaac tgagtcaaga tctgaaatgt agagatgatc 360
tctgacgata cctgtatgtt cttattgtgt aaataaaaatt gctggtatga aatgaca 417

```

<210> 190

<211> 497

<212> DNA

<213> Homo sapiens

<400> 190

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gcactgcggc gctctcccgt cccgcgggtg ttgctgctgc tgccgctgct gctgggcctg 60
aacgcaggag ctgtcattga ctggcccaca gaggagggca aggaagtatg ggattatgtg 120
acgggtccgca aggatgccta catgttcttg ttgctctatt atgccaccaa ctctgcaag 180
aactttctcag aactgcccct ggtcatgttg cttcaggggc gtccaggcgg ttctagcact 240
ggatttgga aacttgagga aattggggcc cttgacagtg atctcaaacc acggaaaacc 300
acctggctcc aggctgccag tctcctatct gtggataatc ccgtgggcac tgggttcagt 360
tatgtgaatg gtagtggtgc ctatgccaa gacctggcta tgggtgcttc agacatgatg 420
gttctcctga agaccttctt cagttgccac aaagaattcc agacagttcc attctacatt 480
ttctcagagt cctatgg 497

```

<210> 191
<211> 175
<212> DNA
<213> Homo sapiens

<400> 191
atgttgaata ttttgcttat taactttggt tattgtcttc tccctcgatt agaattattag 60
ctacttgagt acaaggattt gagcctgtta cattcactgc tgaatttttag gctcctggaa 120
gatacccagc attcaataga gaccacacaa taaatatatg tcaaataaaa aaaaa 175

<210> 192
<211> 526
<212> DNA
<213> Homo sapiens

<400> 192
agtaaacatt attatttttt ttatatttgc aaaggaaaca tatctaattcc ttcctataga 60
aagaacagta ttgctgtaat tccttttctt ttcttctca ttctctctgc cccttaaaag 120
attgaagaaa gagaaacttg tcaactcata tccacgttat ctagcaaagt acataagaat 180
ctatcactaa gtaatgtatc cttcagaatg tgttggttta ccagtgcacac cccatattca 240
tcacaaaatt aaagcaagaa gtccatagta atttatttgc taatagtga tttttaatgc 300
tcagagtttc tgagggtcaaa ttttatcttt tcacttacia gctctatgat cttaaataat 360
ttacttaatg tattttggtg tattttcctc aaattaatat tgggtgtcaa gactatatct 420
aattcctctg atcactttga gaaacaaact tttattaatat gtaaggcact tttctatgaa 480
ttttaaatat aaaaataaat attgttctga ttattactga aaaaaa 526

<210> 193
<211> 553
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (290)
<223> n=A,T,C or G
<221> unsure
<222> (300)
<223> n=A,T,C or G
<221> unsure
<222> (411)
<223> n=A,T,C or G
<221> unsure
<222> (441)
<223> n=A,T,C or G

<400> 193
tccattgtgg tggaaattcgc tctctggtta aggcgtgcag gtgttgccg cggcctctga 60
gctgggatga gccgtgctcc cgggtggaagc aaggagagccc agccggagcc atggccagta 120
cagtggtagc agttggactg accattgctg ctgcaggatt tgcaaggcgt tacgttttgc 180
aagccatgaa gcatatggag cctcaagtaa aacaagtttt tcaaagccta ccaaaatctg 240
ccttcagtgg tggctattat agagggtgggt ttgaacccaa aatgacaaan cgggaagcan 300
cattaatact aggtgtaagc cctactgccca ataaaggga aataagagat gctcatcgac 360
gaattatgct tttaaatcat cctgacaaag gaggatctcc ttatatagca nccaaaatca 420
atgaagctaa agatttacta naagggtcaag ctaaaaaatg aagtaaatgt atgatgaatt 480

ttaagttcgt attagtttat gtatatgagt actaagtttt tataataaaa tgcctcagag 540
ctacaatttt aaa 553

<210> 194

<211> 320

<212> DNA

<213> Homo sapiens

<400> 194

cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgttt cccaacaggg 60
atgtcacttg atatgagaat ctcaaattct aatgccttat aagcattcct tcctgtgtcc 120
attaagactc tgataattgt ctccctccca taggaatttc tcccaggaaa gaaatatatc 180
cccatctccg tttcatatca gaactaccgt ccccgatatt cccttcagag agattaaaga 240
ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcct attttcttcc 300
attgacccat atttatacct 320

<210> 195

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (203)

<223> n=A,T,C or G

<221> unsure

<222> (218)

<223> n=A,T,C or G

<400> 195

aagcatgacc tggggaaatg gtcagacctt gtatttgtgt tttggccttg aaagtagcaa 60
gtgaccagaa tctgccatgg caacaggctt taaaaaagac ccttaaaaag acactgtctc 120
aactgtgggt ttagcaccag ccagctctct gtacatttgc tagctttag ttttctaaga 180
ctgagtaaac ttcttatttt tanaaagggg aggctggntt gtaactttcc ttgtacttaa 240
ttgggtaaaa gtcttttcca caaaccacca tctattttgt gaactttgtt agtcatcttt 300
tatttggtaa attatgaact 320

<210> 196

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (36)

<223> n=A,T,C or G

<400> 196

atataaaaata atacgaaact ttaaaaagca ttggantgtc agtatgttga atcagtagtt 60
tcactttaac tgtaaacaaat ttcttaggac accatttggg ctagtctctg tgtaagtgtg 120
aatactacaa aaacttattt atactgttct tatgtcattt gttatattca tagatttata 180
tgatgatatg acatctggct aaaaagaaat tattgcaaaa ctaaccacta tgtacttttt 240
tataaatact gtatggacaa aaaatggcat tttttatatt aaattgttta gctctggcaa 300
aaaaaaaaa ttttaagagc tgggtactaat aaaggattat tatgactggt aaaaaaa 357

<210> 197
 <211> 565
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (27)
 <223> n=A,T,C or G

<400> 197
 tcagctgagt accatcagga tatttanccc ttttaagtgt gttttgggag tagaaaacta 60
 aagcaacaat acttcctctt gacagctttg attggaatgg ggttattaga tcattcacct 120
 tggctctaca ctttttagga tgcttggtga acataacacc acttataatg aacatccctg 180
 gttcctatat tttgggctat gtgggtagga attgttactt gttactgcag cagcagccct 240
 agaaagtaag ccagggcctt cagatctaag ttagtccaaa agctaaatga tttaaagtca 300
 agttgtaatg ctaggcataa gcactctata atacattaaa ttataggccg agcaattagg 360
 gaatgtttct gaaacattaa acttgatatt atgtcactaa aattctaaca caaacttaaa 420
 aaatgtgtct catacatatg ctgtactagg cttcatcatg catttctaaa tttgtgtatg 480
 atttgaatat atgaaagaat ttatacaaga gtgttattta aaattattaa aaataaatgt 540
 atataatttg tacctattgt aaaaa 565

<210> 198
 <211> 484
 <212> DNA
 <213> Homo sapiens

<400> 198
 tatgtaagta ttggtgtctg ctttaaaaaa ggagaccag acttcacctg tcctttttta 60
 acatttgaga acagtgttac tctgagcagt tgggccacct tcaccttata cgacagctga 120
 ctgttgatg tgtccattgt cgccagtttg gctgttgccc ggacaggaca ggacctccat 180
 tgggcgcagc agcaggtggc aggggtgtgg cttgaggtgg gtggcagcgt ctggtcctcc 240
 tctctggtgc tttctgagag ggtctctaaa gcagagtgtg gttggcctgg ggggaaggcag 300
 agcacgtatt tctccctct agtacctctg catttgtgag tgttccctct ggccttctga 360
 agggcagcag actcttgagt atactgcaga ggacatgctt tatcagtagg tcctgagggc 420
 tccaggggct caactgacca agtaacacag aagttggggt atgtggccta tttgggtcgg 480
 aaac 484

<210> 199
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (77)
 <223> n=A,T,C or G
 <221> unsure
 <222> (88)
 <223> n=A,T,C or G
 <221> unsure
 <222> (134)
 <223> n=A,T,C or G
 <221> unsure
 <222> (151)

<223> n=A,T,C or G
 <221> unsure
 <222> (189)
 <223> n=A,T,C or G
 <221> unsure
 <222> (227)
 <223> n=A,T,C or G
 <221> unsure
 <222> (274)
 <223> n=A,T,C or G
 <221> unsure
 <222> (319)
 <223> n=A,T,C or G

<400> 199
 gcttatgttt tttgttttaa cttttgtttt ttaacattta gaatattaca ttttgtatta 60
 tacagtaect ttctcanaca ttttgtanaa ttcatttcgg cagctcacta ggattttgct 120
 gaacattaaa aagngtgata gcgatattag ngccaatcaa atggaaaaaa ggtagtctta 180
 ataaacaana cacaacgttt ttatacaaca tactttaaaa tattaanaaa actccttaat 240
 attgtttcct attaagtatt attctttggg caanattttc tgatgctttt gattttctct 300
 caatttagca tttgctttng gtttttttct ctatttagca ttctgttaag gcacaaaaac 360
 tatgtactgt atgggaaatg ttgtaaatat taccttttcc acatttttaa cagacaactt 420
 tgaatccaa 429

<210> 200
 <211> 279
 <212> DNA
 <213> Homo sapiens

<400> 200
 gcttttttga ggaattacag ggaagctcct ggaattgtac atggatatct ttatccctag 60
 ggggaaatca aggagctggg caccctaat tctttatgga agtgttttaa actattttta 120
 ttttattaca agtattacta gagtagtggg tctactctaa gatttcaaaa gtgcatttaa 180
 aatcatatcat gttccgcct gcaaataat tggtattttg gtggagaaaa aaatagtata 240
 ttctacataa aaaattaaag atattaacta agaaaaaaa 279

<210> 201
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 201
 taggtcagta ttttttagaaa ctcttaatag ctcatactct tgataccaaa agcagccctg 60
 attgttaaag cacacacctg cacaagaagc agtgatgggt gcattttacat ttctgggtg 120
 cacaaaaaaa aattctcaaa aagcaaggac ttacgctttt tgcaaagcct ttgagaagtt 180
 actggatcat aggaagctta taacaagaat ggaagattct taaataactc actttctttg 240
 gtatccagta acagtagatg ttcaaaatat gtagctgatt aataccagca ttgtgaacgc 300
 tgtacaacct tgtgggttatt actaagcaag ttactactag cttctgaaaa gtagcttcat 360
 aattaatggt atttatacac tgccttccat gacttttact ttgccttaag ctaatctcca 420
 aaatctgaaa tgctactcca atatcagaaa aaaaggggga ggtggaatta tatttctgt 480
 gattttaaga gtacagagaa tcatgcacat ctctgattag ttcatatatg tctagtgtgt 540
 aataaaagtc aaagatgaac tctcaaaaa 569

<210> 202
 <211> 501

<212> DNA

<213> Homo sapiens

<400> 202

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attaataggc ttaataattg ttggcaagga tccttttggc ttctttggca tgcaagctcc 60
tagcatctgg cagtggggcc aagaaaataa ggtttatgca tgtatgatgg ttttcttctt 120
gagcaacatg attgagaacc agtgtatgtc aacagggtgca tttagataa ctttaaataa 180
tgtacctgtg tgggtctaagc tggaaatctg tcaccttcca tccatgcaac aacttggtca 240
aattcttgac aatgaaatga agctcaatgt gcatatggat tcaatccac accatcgatc 300
atagcaccac ctatcagcac tgaaaactct tttgcattaa gggatcattg caagagcagc 360
gtgactgaca ttatgaaggc ctgtactgaa gacagcaagc tgtagtaca gaccagatgc 420
tttcttggca ggctcgttgt acctcttgga aaacctcaat gcaagatagt gtttcagtgc 480
tggcatattt tgggaattctg c 501
```

<210> 203

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (36)

<223> n=A,T,C or G

<221> unsure

<222> (96)

<223> n=A,T,C or G

<400> 203

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gacaagctcc tggctctgag atgtcttctc gttaangaga tgggcctttt ggaggtaaag 60
gataaaatga atgagttctg tcatgattca ctattntata acttgcatga cctttactgt 120
gttagctctt tgaatgttct tgaaatttta gactttcttt gtaaacaat gatatgtcct 180
tatcattgta taaaagctgt tatgtgcaac agtgtggaga ttccttgtct gatttaataa 240
aataacttaa cactgaaaaa a 261
```

<210> 204

<211> 421

<212> DNA

<213> Homo sapiens

<400> 204

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agcatctttt ctacaacgtt aaaattgcag aagtagctta tcattaaaaa acaacaacaa 60
caacaataac aataaatcct aagtgtaaat cagttattct accccctacc aaggatatca 120
gcctgttttt tccctttttt ctccctggga taattgtggg cttcttcca aatttctaca 180
gcctctttcc tcttctcatg cttgagcttc cctgtttgca cgcatgcgtg tgcaggactg 240
gcttggtgtg ttggactcgg ctccagggtg aagcatgctt tcccttggtta ctgttgagaga 300
aactcaaac ttcaagccct aggtgtagcc attttgtcaa gtcataaact gtatttttgt 360
actggcatta acaaaaaaag aagataaaat attgtacat taaacttta taaaacttta 420
a 421
```

<210> 205

<211> 460

<212> DNA

<213> Homo sapiens

<400> 205


```

tactctcaca atgaaggacc tggaatgaaa aatctgtgtc taaacaagtc ctcttttagat 60
tttagtgcaa atccagagcc agcgtcgggt gcctcgagta attctttcat gggtagcctt 120
ggaaaagctc tcaggagacc tcacctagat gcctattcaa gctttggaca gccatcagat 180
tgtcagccaa gagcctttta tttgaaagct cattcttccc cagacttgga ctctgggtca 240
gaggaagatg ggaaagaaa gacagatttt caggaagaaa atcacatttg tacctttaaa 300
cagactttag aaaactacag gactccaaat tttcagtctt atgacttgga cacatagact 360
gaatgagacc aaaggaaaag cttaacatac tacctcaagg tgaactttta tttaaaagag 420
agagaatctt atgtttttta aatggagtta tgaattttta 460

```

<210> 206

<211> 481

<212> DNA

<213> Homo sapiens

<400> 206

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tgtgttgga ttcgggacgc cccagagacc tgactttttc ctgcgtgggc cgtctcctcc 60
tgcggaagca gtgacctctg acccctgggtg accttcgctt tgagtgcctt ttgaacgctg 120
gtcccgcggg acttggtttt ctcaagctct gtctgtccaa agacgctccg gtcgagggtc 180
cgctgcctt ggggtggatac ttgaacccca gacgcccctc tgtgtctgtg tgcgcggagg 240
cggccttccc atctgcctgc ccaccggag ctctttccgc cggcgcaggg tcccaagccc 300
acctccgcgc ctgagtcctg cgggtgtgct ctgggcacgt cctgcacaca caatgcaagt 360
cctggcctcc gcgcccgcgc gccacgcga gccgtaccgc ccgccaactc tgttatttat 420
gggtgtgacct cctggagggtg ccctcggccc accggggcta tttattgttt aatttatttg 480
t 481

```

<210> 207

<211> 605

<212> DNA

<213> Homo sapiens

<400> 207

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accttttttg gattcagggc tcctcacaat taaaatgagt gtaatgaaac aagggtgaaaa 60
tatagaagca tccctttgta tactgttttg ctacttacag tgtacttggc attgctttat 120
ctcactggat tctcacggta ggatttctga gatcttaatc taagctccaa agttgtctac 180
ttttttgatc ctaggggtgt ccttttggtt tacagagcag ggtcacttga tttgctagct 240
gggtggcagaa ttggcaccat taccaggtc tgactgacca ccagtcagag gcactttatt 300
tgtatcatga aatgatttga aatcattgta aagcagcgaa gtctgataat gaatgccagc 360
tttccttggt ctttgataac aaagactcca aatattcttg agaacctgga taaaagtgtg 420
aagggtctaga ttgggatttg aagacaaaat tgtaggaaat cttacatttt tgcaataaca 480
aacattaatg aaagcaaaac attataaaag taattttaat tcaccacata cttatcaatt 540
tcttgatgct tccaaatgac atctaccaga tatggttttg tggacatctt tttctgttta 600
cataa 605

```

<210> 208

<211> 655

<212> DNA

<213> Homo sapiens

<400> 208

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ggcgttggtc tggattcccg tcgtaactta aagggaaact ttcacaatgt ccggagccct 60
tgatgtcctg caaatgaagg aggaggatgt ccttaagttc cttgcagcag gaaccactt 120
aggtggcacc aatcttgact tcagatgga acagtacatc tataaaagga aaagtgtatg 180
catctatatc ataaatctca agaggacctg ggagaagctt ctgctggcag ctctgtgcaat 240
tgttgccatt gaaaaccctg ctgatgtcag tgttatatcc tccaggaata ctggccagag 300
ggctgtgctg aagtttgctg ctgccactgg agccactcca attgctgggc gcttcaactc 360

```

tggaaccttc actaaccaga tccaggcagc cttccgggag ccacggcttc ttgtgggttac 420
tgacccacagg gctgaccacc agcctctcac ggaggcatct tatgttaacc tacctaccat 480
tgcgctgtgt aacacagatt ctctctgcg ctatgtggac attgccatcc catgcaacaa 540
caagggagct cactcagtgg gtttgatgtg gtggatgctg gctcgggaag ttctgcgcac 600
gcgtggcacc atttcccgctg aacacccatg ggaggtcatg cctgatctgt acttc 655

<210> 209

<211> 621

<212> DNA

<213> Homo sapiens

<400> 209

catttagaac atggttatca tccaagacta ctctaccctg caacattgaa ctccaagag 60
caaatccaca ttctcttga gttctgcagc ttctgtgtaa atagggcagc tgcgtctat 120
gccgtagaat cacatgatct gaggaccatt catggaagct gctaaatagc ctagtctggg 180
gagtcttcca taaagttttg catggagcaa acaaacagga ttaaaactagg tttggttcct 240
tcagccctct aaaagcatag ggcttagcct gcaggcttcc ttgggctttc tctgtgtgtg 300
tagttttgta aacactatag catctgtaa gatccagtgt ccatggaaac cttcccacat 360
gccgtgactc tggactatat cagtttttgg aaagcagggt tcctctgcct gctaacaagc 420
ccacgtggac cagtctgaat gtctttcctt tacacctatg tttttaata gtcaaaacttc 480
aagaaacaat ctaaacaagt ttctgttgca tatgtgtttg tgaacttgta tttgtattta 540
gtaggcttct atattgcatt taacttgttt ttgtaactcc tgattcttcc ttttcggata 600
ctattgatga ataaagaaat t 621

<210> 210

<211> 533

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (20)

<223> n=A,T,C or G

<221> unsure

<222> (21)

<223> n=A,T,C or G

<221> unsure

<222> (61)

<223> n=A,T,C or G

<400> 210

cgccttgagg agccggcggn ngagtccggg acgtggagac ccgggggtccc ggcagccggg 60
nggcccgcgg gccaggggtg gggatgcacc gccgcggggt gggagctggc gccatcgcca 120
agaagaaact tgcagaggcc aagtataagg agcgaggagc ggtcttggct gaggaccagc 180
tagcccagat gtcaaagcag ttggacatgt tcaagaccaa cctggaggaa tttgccagca 240
aacacaagca ggagatccgg aagaatcctg agttccgtgt gcagttccag gacatgtgtg 300
caaccattgg cgtggatccg ctggcctctg gaaaaggatt ttggtctgag atgctgggcg 360
tgggggactt ctattacgaa ctaggtgtcc aaattatcga agtgtgcctg gcgctgaagc 420
atcggaatgg aggtctgata actttggagg aactacatca acaggtgttg aagggaaggg 480
gcaagtccgc ccaggatgtc agtcaagatg acctgatcag agccatcaag aaa 533

<210> 211

<211> 451

<212> DNA

<213> Homo sapiens

<400> 211
 ttagcttgag cccgagaacga ggcgagaaaag ctggagaccg aggagaccgc ctagagcgga 60
 gtgaacgggg aggggaccgt ggggaccggc ttgatcgtgc gcggacacct gctaccaagc 120
 ggagcttcag caaggaagtg gaggagcgga gtagagaacg gccctcccag cctgaggggc 180
 tgcgcaaggc agctagcctc acggaggatc gggaccgtgg gcgggatgcc gtgaagcgag 240
 aagctgcctc acccccagtg agccccctga aggcggctct ctctgaggag gagttagaga 300
 agaaatccaa ggctatcatt gaggaatata tccatctcaa tgacatgaaa gaggcagtcc 360
 agtgcgtgca ggagctggcc tcacctcct tgctcttcat ctttgtagcg catggtgtcg 420
 agtctacgct ggagcgcagt gccattgctc g 451

<210> 212
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220> .
 <221> unsure
 <222> (54)
 <223> n=A,T,C or G

<400> 212
 gtgattattc ttgatcaggg agaagatcat ttagatttgt tttgcattcc ttanaatgga 60
 gggcaacatt ccacagctgc cctggctgtg atgagtgtcc ttgcaggggc cggagtagga 120
 gcactggggg gggggcgga ttggggttac tcgatgtaag ggattccttg ttgttgtgtt 180
 gagatccagt gcagttgtga tttctgtgga tcccagcttg gttccaggaa ttttgtgtga 240
 ttggcttaaa tccagttttc aatcttcgac agctgggctg gaacgtgaac tcagtagctg 300
 aacctgtctg acccggtcac gttcttgat cctcagaact ctttgctctt gtcgggggtg 360
 ggggtgggaac tcacgtgggg agcgggtgct gagaaaatgt aaggattctg gaatacatat 420
 tccatgggac tttccttccc tctcctgctt cctcttttcc tgctccctaa c 471

<210> 213
 <211> 511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (27)
 <223> n=A,T,C or G
 <221> unsure
 <222> (63)
 <223> n=A,T,C or G
 <221> unsure
 <222> (337)
 <223> n=A,T,C or G
 <221> unsure
 <222> (442)
 <223> n=A,T,C or G

<400> 213
 ctaattagaa acttgctgta cttttntttt tcttttaggg gtcaaggacc ctctttatag 60
 ctncatttg cctacaataa attattgcag cagtttgcaa tactaaaata ttttttatag 120
 actttatatt tttccttttg ataaaggat gctgcatagt agagttggtg taattaaact 180
 atctcagccg tttcctgct ttccttctg ctccatagc ctcatgtcc ttccaggag 240

```

ctcttttaaat cttaaagttc tacatttcat gctcttagtc aaattctggt accttttttaa 300
taactcttcc cactgcataat ttccatcttg aattggnggt tctaaattct gaaactgtag 360
ttgagataca gctattttaat atttctggga gatgtgcac cctcttcttt gtggttgccc 420
aaggttggtt tgcgtaactg anaactccttg atatgcttca gagaatttag gcaaactg 480
gccatggccg tgggagtact gggagtaaaa t 511

```

```

<210> 214
<211> 521
<212> DNA
<213> Homo sapiens

```

```

<400> 214
agcattgccca aataatccct aattttccac taaaaatata atgaaatgat gttaagcttt 60
ttgaaaagtt taggttaaac ctactgttgt tagattaatg tatttggtgc ttccctttat 120
ctggaatgtg gcattagctt ttttatttta accctcttta attcttattc aattccatga 180
cttaagggtg gagagctaaa cactgggatt tttggataac agactgacag ttttgcataa 240
ttatdatcgg cattgtacat agaaaggata tggctacctt ttgttaaate tgcactttct 300
aaatatcaaa aaagggaat gaagtataaa tcaatttttg tataatctgt ttgaaacatg 360
agtttttattt gcttaatat agggctttgc cccttttctg taagtctctt gggatcctgt 420
gtagaagctg ttctcattaa acaccaaaca gttaagtcca ttctctggta ctagctacaa 480
attcggtttc atattctact taacaattta aataaactga a 521

```

```

<210> 215
<211> 381
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> unsure
<222> (17)
<223> n=A,T,C or G
<221> unsure
<222> (20)
<223> n=A,T,C or G
<221> unsure
<222> (60)
<223> n=A,T,C or G
<221> unsure
<222> (61)
<223> n=A,T,C or G
<221> unsure
<222> (365)
<223> n=A,T,C or G

```

```

<400> 215
gagcggagag cggaccngtn agagccctga gcagcccccac cgccgcccgc ggcctagttt 60
ncatcacacc ccgggaggag ccgcagctgc cgcagccggc ccagtcacc atcacgcaa 120
ccatgagcag cgaggccgag acccagcagc cgcccgcgc cccccccgccc gccccgcgcc 180
tcagcgccgc cgacaccaag cccggcacta cgggcagcgg cgcagggagc ggtggccgg 240
gcgccctcac atcgcgggc cctgccggcg gggacaagaa ggtcatcgca acgaagggtt 300
tggaacagt aaaatggttc aatgtaagga acggatatgg ttcatcaac aggaatgaca 360
ccaangaaga tgtatttga c 381

```

```

<210> 216
<211> 425

```

<212> DNA

<213> Homo sapiens

<400> 216

```

ttactaacta ggtcattcaa ggaagtcaag ttaacttaaa catgtcacct aaatgcactt 60
gatgggtgttg aaatgtccac cttctttaa ttttaagatg aacttagttc taaagaagat 120
aacaggccaa tcctgaagggt actccctggt tgctgcagaa tgtcagatat tttggatggt 180
gcataagagt cctatttgcc ccagttaatt caacttttgt ctgctgttt tgtggactgg 240
ctggctctgt tagaactctg tccaaaaagt gcatggaata taacttgtaa agcttccac 300
aattgacaat atatatgcat gtgtttaaac caaatccaga aagcttaaac aatagagctg 360
cataatagta tttattaaag aatcacaact gtaaactga gaataactta aggattctag 420
tttag                                           425

```

<210> 217

<211> 181

<212> DNA

<213> Homo sapiens

<400> 217

```

gagaaaccaa atgatagggt gtagagcctg atgactccaa acaaagccat caccgcatt 60
cttctcctt cttctggtgc tacagctcca agggcccttc accttcatt ctgaaatgga 120
actttggctt tttcagtga agaatatgtt gaaggtttca tttgttcta gaaaaaaaaa 180
a                                           181

```

<210> 218

<211> 405

<212> DNA

<213> Homo sapiens

<400> 218

```

caggccttcc agttcactga caaacatggg gaagtgtgcc cagctggctg gaaacctggc 60
agtataacca tcaagcctga tgtccaaaag agcaaagaat atttctccaa gcagaagtga 120
gagctgggct gttttagtgc caggctgcgg tgggcagcca tgagaacaaa acctcttctg 180
tatttttttt ttccattagt aaaacacaag acttcagatt cagccgaatt gtggtgtctt 240
acaaggcagg cctttcctac aggggggtgga gagaccagcc tttctcctt tggtaggaat 300
ggcctgagtt ggcgtgtggt gcaggctact ggtttgtatg atgtattagt agagcaacc 360
attaatcttt tgtagtttgt attaaacttg aactgagaaa aaaaa 405

```

<210> 219

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (207)

<223> n=A,T,C or G

<221> unsure

<222> (210)

<223> n=A,T,C or G

<400> 219

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actccaagag ttagggcagc agagtggagc gatttagaaa gaacatttta aaacaatcag 60
ttaatttacc atgtaaaatt gctgtaaatg ataatgtgta cagattttct gttcaaatat 120
tcaattgtaa acttcttgtt aagactgtta cgtttctatt gcttttgtat gggatattgc 180

```

aaaaataaaa aggaaagaac cctcttnaan aaaaaa

216

<210> 220

<211> 380

<212> DNA

<213> Homo sapiens

<400> 220

cttacaaatt gcccccatgt gtaggggaca cagaaccctt tgagaaaact tagatttttg 60
tctgtacaaa gtctttgcct ttttccttct tcattttttt ccagtacatt aaatttgtca 120
atttcattctt tgagggaac tgattagatg ggttgtgttt gtgttctgat ggagaaaaca 180
gcacccaag gactcagaag atgattttta cagttcagaa cagatgtgtg caatattggg 240
gcatgtaata atgttgagtgc gcagtcaaaa gtcattgatt ttatcttagt tcttcattac 300
tgcattgaaa aggaaaacct gtctgagaaa atgcctgaca gtttaattta aaactatggg 360
gtaagtcttt gacaaaaaaa 380

<210> 221

<211> 398

<212> DNA

<213> Homo sapiens

<400> 221

ggttagtaag ctgtcgactt tgtaaaaaag ttaaaaatga aaaaaaagg aaaaatgaat 60
tgtatattta atgaatgaac atgtacaatt tgccactggg aggaggttcc tttttgttgg 120
gtgagctctgc aagtgaattt cactgatgtt gatattcatt gtgtgtagtt ttatttcggg 180
cccagccccg tttcctttta ttttggagct aatgccagct gcgtgtctag ttttgagtgc 240
agtaaaatag aatcagcaaa tcaactcttat ttttcacctt tttccggtat tttttgggtt 300
gtttctgtgg gagcagtgtt caccaactct tctgttatat tgcctttttg ctggaaaatg 360
ttgtatgttg aataaaattt tctataaaaa ttaaaaaa 398

<210> 222

<211> 301

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (49)

<223> n=A,T,C or G

<221> unsure

<222> (64)

<223> n=A,T,C or G

<400> 222

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<210> 223

<211> 200

<212> DNA

<213> Homo sapiens

<400> 223

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<210> 224

<211> 385

<212> DNA

<213> Homo sapiens

<400> 224

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<210> 225

<211> 560

<212> PRT

<213> Homo sapien

<400> 225

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Gly	Asp	Met	Arg	Trp	Lys	Asn	Ser	Trp	Lys	Gly	Arg	Val	Gln	Ala	
65					70				75					80	
Val	Leu	Thr	Ser	Asp	Ser	Pro	Ala	Leu	Val	Gly	Ser	Asn	Ile	Thr	Phe
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Ala	Val	Asn	Leu	Ile	Phe	Pro	Arg	Cys	Gln	Lys	Glu	Asp	Ala	Asn	Gly
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Asn	Ile	Val	Tyr	Glu	Lys	Asn	Cys	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Ala
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Asp	Pro	Tyr	Val	Tyr	Asn	Trp	Thr	Ala	Trp	Ser	Glu	Asp	Ser	Asp	Gly
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Glu	Asn	Gly	Thr	Gly	Gln	Ser	His	His	Asn	Val	Phe	Pro	Asp	Gly	Lys
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Pro	Phe	Pro	His	His	Pro	Gly	Trp	Arg	Arg	Trp	Asn	Phe	Ile	Tyr	Val
			165				170						175		
Phe	His	Thr	Leu	Gly	Gln	Tyr	Phe	Gln	Lys	Leu	Gly	Arg	Cys	Ser	Val
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Arg	Val	Ser	Val	Asn	Thr	Ala	Asn	Val	Thr	Leu	Gly	Pro	Gln	Leu	Met
		195				200						205			
Glu	Val	Thr	Val	Tyr	Arg	Arg	His	Gly	Arg	Ala	Tyr	Val	Pro	Ile	Ala

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Gln Val Lys Asp Val Tyr Val Val Thr Asp Gln Ile Pro Val Phe Val		
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Thr Met Phe Gln Lys Asn Asp Arg Asn Ser Ser Asp Glu Thr Phe Leu		240
	245	250
Lys Asp Leu Pro Ile Met Phe Asp Val Leu Ile His Asp Pro Ser His		255
	260	265
Phe Leu Asn Tyr Ser Thr Ile Asn Tyr Lys Trp Ser Phe Gly Asp Asn		270
	275	280
Thr Gly Leu Phe Val Ser Thr Asn His Thr Val Asn His Thr Tyr Val		285
	290	295
Leu Asn Gly Thr Phe Ser Leu Asn Leu Thr Val Lys Ala Ala Ala Pro		300
305	310	315
Gly Pro Cys Pro Pro Pro Pro Pro Pro Arg Pro Ser Lys Pro Thr		320
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Pro Ser Leu Gly Pro Ala Gly Asp Asn Pro Leu Glu Leu Ser Arg Ile		335
	340	345
Pro Asp Glu Asn Cys Gln Ile Asn Arg Tyr Gly His Phe Gln Ala Thr		350
	355	360
Ile Thr Ile Val Glu Gly Ile Leu Glu Val Asn Ile Ile Gln Met Thr		365
	370	375
Asp Val Leu Met Pro Val Pro Trp Pro Glu Ser Ser Leu Ile Asp Phe		380
385	390	395
Val Val Thr Cys Gln Gly Ser Ile Pro Thr Glu Val Cys Thr Ile Ile		400
	405	410
Ser Asp Pro Thr Cys Glu Ile Thr Gln Asn Thr Val Cys Ser Pro Val		415
	420	425
Asp Val Asp Glu Met Cys Leu Leu Thr Val Arg Arg Thr Phe Asn Gly		430
	435	440
Ser Gly Thr Tyr Cys Val Asn Leu Thr Leu Gly Asp Asp Thr Ser Leu		445
	450	455
Ala Leu Thr Ser Thr Leu Ile Ser Val Pro Asp Arg Asp Pro Ala Ser		460
465	470	475
Pro Leu Arg Met Ala Asn Ser Ala Leu Ile Ser Val Gly Cys Leu Ala		480
	485	490
Ile Phe Val Thr Val Ile Ser Leu Leu Val Tyr Lys Lys His Lys Glu		495
	500	505
Tyr Asn Pro Ile Glu Asn Ser Pro Gly Asn Val Val Arg Ser Lys Gly		510
	515	520
Leu Ser Val Phe Leu Asn Arg Ala Lys Ala Val Phe Phe Pro Gly Asn		525
	530	535
Gln Glu Lys Asp Pro Leu Leu Lys Asn Gln Glu Phe Lys Gly Val Ser		540
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		560

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<211> 9

<212> PRT

<213> Homo sapien

<400> 226

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1

5

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<212> PRT
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<400> 229
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1 5 10

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Arg Leu Thr Gly Gly Leu Lys Phe Phe Val
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<210> 231
<211> 9
<212> PRT
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<400> 231
Ser Leu Gln Ala Leu Lys Val Thr Val
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<210> 232
<211> 20
<212> PRT
<213> Homo sapiens

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Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr Ser Arg Tyr Phe
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Phe Ser Phe Ala
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<213> Homo sapiens

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Asn His Ser Pro Ser
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<210> 234
<211> 20
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Asp Pro Asp Gly
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Pro Asn Ser Asp
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Asn Pro Gln Gln
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<210> 237

<211> 21
<212> PRT
<213> Homo sapiens

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Phe Ile Pro Pro Asn
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<210> 238
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Thr His Glu Ser His Arg Ile Tyr Val Ala Ile Arg Ala Met Asp Arg
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Gln Ile Ser Thr
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Ile Gln Asp Asp Phe
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<210> 241
<211> 20
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<400> 241

Glu Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser
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Val Leu Gly Val
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<210> 242

<211> 20

<212> PRT

<213> Homo sapiens

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Gln Met Asn Ala
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<210> 243

<211> 20

<212> PRT

<213> Homo sapiens

<400> 243

Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile Pro Gly
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Ser His Ala Met
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<210> 244

<211> 20

<212> PRT

<213> Homo sapiens

<400> 244

Ala Val Pro Pro Ala Thr Val Glu Ala Phe Val Glu Arg Asp Ser Leu
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His Phe Pro His
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<210> 245

<211> 20

<212> PRT

<213> Homo sapiens

<400> 245

Lys Pro Gly His Trp Thr Tyr Thr Leu Asn Asn Thr His His Ser Leu

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<211> 20			
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<400> 246			
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Pro Gly His Trp			
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Phe Tyr Pro Ile			
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<210> 248			
<211> 20			
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Leu Thr Phe Arg
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Val Pro Pro Ala
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 35 40 45
 Ala Ala Val Ser Ser Ile Phe Asn Ser Pro Glu Glu Phe Leu Gly Lys
 50 55 60
 Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65 70 75 80
 Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Ile Thr
 85 90 95
 Pro Glu Ala Phe Glu Lys Leu Gly Phe Pro Ala Ala Lys Glu Ile Ala
 100 105 110
 Asn Met Cys Arg Phe Tyr Glu Met Lys Pro Asp Arg Asp Val Asn Leu
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 145 150

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 <213> Homo sapien

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agctgtaaaa	gtagaagagg	aattgaccct	atcttgagca	gcacctggag	aagactttga	7380
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tgacttttaac	aatgctattt	tagtaaatac	atcaaagcga	aatcctcagc	aagctggcat	7500
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tcctgtacct	gccagagatt	atcttatatt	gaaaggagtt	ttaacagcaa	tgggtttgat	7740
aggaatcatt	tgcttatta	tagttgtgac	acatcatact	ttaagcagga	aaaagagagc	7800
agacaagaaa	gagaatggaa	caaaattatt	ataatgaatt	ctgcagatat	ccatcacact	7860
ggcgcccgct	cgagcaccac	caccaccacc	actgagatcc	ggctgctaac	aaagcccgaa	7920
aggaagctga	gttggctgct	gccaccgctg	agcaataact	agcataaccc	cttggggcct	7980
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<210> 255

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 255

gtggccagng actagaaggc gagggcgccgc gggaccatgg cggcgggcggc ggacgagcgg	60
agtccanagg acggagaaga cgaggaagag gaggagcagt tggttctggt ggaattatca	120
ggaattattg attcagactt cctctcaaaa tgtgaaaata aatgcaagg tttgggcatt	180
gacactgaga ggccattct gcaagtggac agctgtgtct ttgctgggga gtatgaagac	240
actctangga cctgtgttat atttgaagaa aatgntnaac atgctgatac agaaggcaat	300
aataaacag tgctaaaata taaatgccat acaatgaaga agctcagcat gacaagaact	360
ctcctgacag agaagaagga aggagaagaa aacatangtg g	401

<210> 256

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 256

tgggtgncct gggatgggga accgcgggtg cttccgngga ggtttcggca ntggcatccg	60
gggcgggggt cgcggccgng gacggggccg gggccnangc cgnnganctc gcggangcaa	120
ggccgaggat aaggagtga tgcccgctcac caacttgggc cgcttgacca aggacatgaa	180
nancaagccc ctgnaggaga tctatntctt cttccctgcc ccattaagga atcaagagat	240
catttgattt cttcctgggg gcctctctca aggatnagg ttttgaagat tatgccagt	300
canaaannan accccgttgc ccngtccatc tncaccaac ncttccaagg gcnatttttg	360
tttaggcctc attncngggg ggaaccttaa cccaatttgg g	401

<210> 257

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 257

atgtatgtaa aacacttcat aaaatgtaa gggctataac aaatatgtta taaagtgatt	60
ctctcagccc tgaggatatac agaatcattt gcctcagact gctgttggat tttaaaattt	120
ttaaaatata tgctaagtaa tttgctatgt cttctccac actatcaata tgctgtcttc	180
taacaggctc cccactttct tttaatgtgc tgttatgagc tttggacatg agataaccgt	240
gcctgttcag agtgtctaca gtaagagctg gacaaactct ggagggacac agtctttgag	300
acagctcttt tggttgcttt ccactttctt gaaaggttca cagtaacctt ctagataata	360
gaaactccca gttaaagcct angctancaa ttttttttag t	401

<210> 258

<211> 401

<212> DNA

<213> Homo sapien

<400> 258

ggagcgctag gtcggtgtac gaccgagatt aggggtgcgtg ccagctccgg gaggccgcgg	60
tgaggggccc ggcccaagct gccgaccga gccgatcgtc agggtcgcca gcgcctcagc	120
tctgtggagg agcagcagta gtcggagggt gcaggatatt agaaatggct actccccagt	180
caattttcat ctttgcaatc tgcattttta tgataacaga attaatctcg gcctcaaaaa	240
gctactatga tatcttaggt gtgccaaaat cggcatcaga gcgccaaatc aagaaggcct	300
ttcacaagtt ggccatgaag taccaccctg acaaaaataa gaccagatg ctgaagcaaa	360
attcagagag attgcagaag catatgaaac actctcagat g	401

<210> 259

<211> 401

<212> DNA

<213> Homo sapien

<400> 259

attgggtttg gagggaggat gatgacagag gaatgccctt tggccatcac ggttttgatt	60
ctccagaata ttgtgggttt gatcatcaat gcagtcatgt taggctgcat tttcatgaaa	120
acagctcagg ctcacagaag gccagaaact ttgattttca gccgccatgc tgtgattgcc	180
gtccgaaatg gcaagctgtg cttcatgttc cgagtgggtg acctgaggaa aagcatgac	240
attagtgcct ctgtgcgcac ccagggtgtc aagaaaacaa ctacacctga aggggaggtg	300
gttcctatc accaactgga cattcctgtt gataacccaa tcgagagcaa taacattttt	360
ctggtggccc ctttgatcat ctgccacgtg attgacaagc g	401

<210> 260

<211> 363

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(363)

<223> n = A,T,C or G

<400> 260

aggaganang gagggggana tgaatagga tggagaggga natagtggat gagcaggga	60
canggagagg aancagaaag gagaggcaag acaggagagac acacancaca nangangana	120
caggtggggg ctgggtggg gcatggagag cctttngant cncacaggcc accctgctct	180
cgctgggctg ttgaaaccca ctccatggct tctgccact gcagttgggc ccagggtgtg	240
cttatnctg gaatgcaagt ggctgtggct tggagcctcc cctctggnnn anggaaannn	300
attgctccct tatctgcttg gaatatctga gtttttccan cccggaaata aaacacacac	360
aca	363

<210> 261

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 261

cggtctccg ccgtctccc ggggtttcgg ggcacttggg tcccacagtc tggctctgct	60
tcaccttccc ctgacctgag tagtcgccat ggcacaggtt ctgagaggca ctgngactga	120

```

cttcctgga tttgatgagc gggctgatgc anaaactctt cggaaggcta tgaaaggctt 180
gggcacagat gaggagagca tcctgactct gttgacatcc cgaagtaatg ctcagcgcca 240
ggaaatctct gcagctttta agactctgtt tggcagggat cttctggatg acctgaaatc 300
agaactaact ggaaaatttg aaaaattaat tgtggctctg atgaaaccct ctcggcttta 360
tgatgcttat gaactgaaac atgccttgaa gggagctgga a 401

```

```

<210> 262
<211> 401
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (401)
<223> n = A,T,C or G

```

```

<400> 262
agtctanaac atttctaata ttttngcgtt tcatatatca aaggagatta tgtgaaacta 60
tttttaata ctgtaaagtg acatatagtt ataagatata tttctgtaca gtagagaaaag 120
agttttataac atgaagaata ttgtaccatt atacattttc attctcgatc tcataagaaa 180
ttcaaaaagaa taatgataga ggtgaaaata tgtttacttt ctctaaatca agcctagtgt 240
tcaactcaaa aattatgntg catagtttta ttttgaattt aggttttggg actacttttt 300
tccancttca atgagaaaat aaaatctaca actcaggagt tactacagaa gttctaanta 360
tttttttgct aannagcnaa aatatataaac atatgaaaat g 401

```

```

<210> 263
<211> 401
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (401)
<223> n = A,T,C or G

```

```

<400> 263
ctgtccgacc aagagaggcc ggccgagccc gaggttggg cttttgcttt ctggcggagg 60
gatctgcggc ggttttaggag gcggcgctga tcctgggagg aagaggcagc tacggcgggc 120
gcggcgggtg cggttagggc ggcggcgaat aaaggggccc cgccgggtg atgcggtgac 180
cactgcggca ggcccaggag ctgagtgggc cccggccctc agcccgctcc gncggacccg 240
ctttcctcaa ctctccatct tctcctgccg accgagatcg ccgaggcggn ctcaggctcc 300
ctanccctt ccccgctcct tcccncccc cgtccccgcc ccggggggccg ccgccacccg 360
cctcccacca tggctctgaa ganaatccac aagggaattga a 401

```

```

<210> 264
<211> 401
<212> DNA
<213> Homo sapien

```

```

<400> 264
aacaccagcc actccaggac cctgaagge ctctaccagg tcaccagtgt tctgcgccta 60
aagccacccc ctggcagaaa cttcagctgt gtgttctgga atactcacgt gagggaaactt 120
actttggcca gcattgacct tcaaagtcag atggaaccca ggacccatcc aacttggtg 180
cttcacattt tcatccctc ctgcacatt gctttcattt tcatagccac agtgatagcc 240
ctaagaaaac aactctgtca aaagctgtat tcttcaaaag acacaacaaa aagacctgtc 300

```

accacaacaa agagggaagt gaacagtgtc gtgaatctga acctgtgggc ttgggagcca 360
gggtgacctg atatgacatc taaagaagct tctggactct g 401

<210> 265
<211> 271
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G

<400> 265
gccacttcct gtggacatgg gcagagcgct gctgccagtt cctggtagcc ttgaccacna 60
cgctgggggg tctttgtgat ggtcatgggt ctcatattgca cttgggggtg tgggattcaa 120
gttagaagtt tctagatctg gccggggcgca gtggctcaca cctgtaatcc cagcacttta 180
ggaggctgag gcaggcggat catgaggtca ggagatcgag accgtcctgg ctaacacagt 240
gaaaccccg tctactaaa aatacaaaaa a 271

<210> 266
<211> 401
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 266
attcataaat ttagctgaaa gatactgatt caatttgtat acagngaata taaatgagac 60
gacagcaaaa ttttcatgaa atgtaaaata tttttatagt ttgttcatac tatatgaggt 120
tctattttaa atgactttct ggatttttaa aaatttcctt aaatacaatc atttttgtaa 180
tattttattt atgcttatga tctagataat tgcagaatat cattttatct gactctgtct 240
tcataagaga gctgtggccg aattttgaac atctgttata gggagtgatc aaattagaag 300
gcaatgtgga aaaacaattc tgggaaagat ttctttatat gaagtccctg ccactagcca 360
gccatcctaa ttgatgaaag ttatctgttc acaggcctgc a 401

<210> 267
<211> 401
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 267
gaagaggcat cacctgatcc cggagacctt tggagttaag aggcggcgga agcgagggcc 60
tgtggagtcg gaccccttc ggggtgagcc agggtcggcg cgcgcggctg tctcanaact 120
catgcagctg ttcccgcgag gcctgtttga ggacgcgctg ccgcccacg tgctgaggag 180
ccaggtgtac agccttgtgc ctgacaggac cgtggccgac cggcagctga aggagcttca 240
agagcanggg gagacaaaat cgtccagctg ggctttnact tggatgccca tggaaanttat 300

tctttcnctt ganggactta cnngggaccc aagaanccct tncaaggggc ccttngtgga 360
 tgggncccgga aaccccnnta tttgcccttg ggggggncca a 401

<210> 268
 <211> 223
 <212> DNA
 <213> Homo sapien

<400> 268
 tcgccatgtt ggccaggctg gtcttgaact cctgacttta agtgatccac ccgcctcaac 60
 ctcccaaagt gctgggatta caggtgtgag ccaccgcgcc tggcctgata catactttta 120
 gaatcaagta gtcacgcact ttttctgttc atttttctaa aaagtaaata tacaaatgtt 180
 ttgttttttg ttttttttgt ttgtttgttt ctgttttttt ttt 223

<210> 269
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 269
 actatgtaaa ccacattgta ctttttttta ctttggcaac aaatatttat acatacaaga 60
 tgctagtcca tttgaatatt tctcccaact tatccaagga tctccagctc taacaaaatg 120
 gtttattttt atttaaagt caatagttgt tttttaaaat ccaaatacaga ggtgcaggcc 180
 accagttaaa tgccgtctat cagggtttgt gccttaagag actacagagt caaagctcat 240
 ttttaaagga gtaggacaaa gttgtcacag gtttttgttg ttgtttttat tgcccccaaa 300
 attacatgtt aatttccatt tatatcaggg attctattta cttgaagact gtgaagttgc 360
 cattttgtct cattgttttc tttgacataa ctaggatcca t 401

<210> 270
 <211> 401
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (401)
 <223> n = A,T,C or G

<400> 270
 tggctgttga ttcacctcag cactgcttgg tatctgcacc ctacctctct ttagaggctg 60
 ccttgtcaac tgaaaaatgc acctgacttc gagcaagact ctttccttag gttctggatc 120
 tgtttgagcc ccatggcact gagctggaat ctgagggctc tgtccaagg atgtgatgat 180
 gtgggagaat gttctttgaa agagcagaaa tccagtctgc atggaaacag cctgtagagn 240
 agaagtttcc agtgataagt gttcactgtt ctaaggaggt acaccacagc tacctgaatt 300
 ttcccaaaat gagtgcttct gtgcgttaca actggccttt gtacttgact gtgatgactt 360
 tgttttttct tttcaattct anatgaacat gggaaaaaat g 401

<210> 271
 <211> 329
 <212> DNA
 <213> Homo sapien

<400> 271
 ccacagcctc caagtcaggt ggggtggagt cccagagctg cacagggttt ggcccaagtt 60
 tctaaggagg gcacttcctc ccctcgcca tcagtgccag ccctgctgg ctggtgctg 120

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agccccctcag acagccccct gccccgcagg cctgccttct cagggacttc tgcggggcct 180
gaggcaagcc atggagttag acccaggagc cggacacttc tcaggaaatg gcttttccca 240
acccccagcc cccacccggt gggtcttcct gttctgtgac tgtgtatagt gccaccacag 300
cttatggcat ctcattgagg acaaaaaaa 329

```

```

<210> 272
<211> 401
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (401)
<223> n = A,T,C or G

```

```

<400> 272
nggctgntaa cntcggaggt nacttcctgg actatcctgg agacccccctc cgcttccacg 60
nncatnatat cntcatngc tgggcccctn angacacnat cccactccaa cacctgngng 120
atgctggncn cctnggaacc ancntcagaa ngacctgnt cntntgtntt ccgcaanctg 180
aagnnaangc gggntacacc tncntgcant ggnccacnct gcnggggaact ntacacacct 240
acgggatgtg gctgcgccan gagccaagag cntttctgga tgattcccca gcctcttgnn 300
agggantcta caacattgct nnntaccttt ntccnncngc nnnntntgga ntacaggngn 360
tnntaacact acatcttttt tactgcncn tncctgggtg g 401

```

```

<210> 273
<211> 401
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (401)
<223> n = A,T,C or G

```

```

<400> 273
cagcaccatg aagatcaaga tcatcgcacc cccagagcgc aagtactcgg tgtggatcgg 60
tggtccatc ctggccctcac tgtccacctt ccagcagatg tggattagca agcaggagta 120
cgacgagtcg ggccccctcca tcgtccaccg caaatgcttc taaacggact cagcagatgc 180
gtagcatttg ctgcatgggt taattgagaa tagaaatttg cccctggcaa atgcacacac 240
ctcatgctag cctcacgaaa ctggaataag ccttcgaaaa gaaattgtcc ttgaagcttg 300
tatctgatat cagcactgga ttgtagaact tggtgctgat tttgaccttg tattgaagtt 360
aactgttccc cttggtatta acgtgtcagg gctgagtgt c 401

```

```

<210> 274
<211> 401
<212> DNA
<213> Homo sapien

```

```

<400> 274
ccacccacac ccaccgcgcc ctctgttcgcc tcttctccgg gagccagtcc gcgccaccgc 60
cgccgcccag gccatcgcca ccctccgcag ccattgtccac caggtcctgt tctctgtcct 120
cctaccgcag gatgttcggc ggcccgggca ccgcgagccg gccgagctcc agccggagct 180
acgtgactac gtccaccgcg acctacagcc tgggcagcgc gctgcgcccc agcaccagcc 240
gcagcctcta cgctctgtcc ccgggcggcg tgtatgccac gcgctcctct gccgtgcgcc 300
tgccggagcag cgtgcccggg gtgcggctcc tgcaggactc ggtggacttc tcgctggccg 360

```

acgccatcaa caccgagttc aagaacaccc gcaccaacga g 401

<210> 275

<211> 401

<212> DNA

<213> Homo sapien

<400> 275

ccacttccac cactttgtgg agcagtgcct tcagcgcaac ccggatgcca ggtatccctg	60
ctggcctggg cctgggcttc gggagagcag aggggtgctca ggagggtaag gccaggggtg	120
gaagggactt acctcccaa ggttctgcag ggggaatctgg agctacacac aggagggatc	180
agctcctggg tgtgtcagag gccagcctgg ggaagctctgg ccactgcttc ccatgagctg	240
agggagaggg agaggggacc cgaggctgag gcataagtgg caggatttcg ggaagctggg	300
gacacggcag tgatgctgag gtctctcctc ccctttccct ccaggcccag tgccagcacc	360
ctcctgaacc actctttctt caagcagatc aagcgacgtg c	401

<210> 276

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 276

tctgatattg ntacccttga gccacctaag ttagaagaaa ttggaaatca agaagttgtc	60
attgttgaag aagcacagag ttcagaagac tttaacatgg gctcttcctc tagcagccag	120
tatactttct gtcagccaga aactgtattt tcctctcagc ctagtgtatga tgaatcaagt	180
agtgtatgaaa ccagtaatca gccagtcct gccttttagac gacgccgtgc taggaagaag	240
accgtttctg cttcagaatc tgaagaccgg ctagtgtgtg aacaagaaac tgaaccttct	300
aaggagttga gtaaacgtca gttcagtagt ggtctcaata agtgtgttat acttgctttg	360
gtgattgcaa tcagcatggg atttgccat ttctatggca c	401

<210> 277

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 277

aactttggca acatatctca gcaaaaacta cagctatggt attcatgcca aaataaaagc	60
tgtgcagagg agtggctgca atgaggtcac aacggtggtg gatgtaaaag agatcttcaa	120
gtcctcatca cccatccctc gaactcaagt cccgctcatt acaaattctt cttgccagt	180
tccacacatc ctgccccatc aagatgttct catcatgtgt tacgagnggc gctcaaggat	240
gatgcttctt gaaaattgct tagttgaaaa atggagagat cagcttagta aaagatccat	300
acagtgggaa gagaggctgc aggaacagcg ganaacagtt caggacaaga agaaaacagc	360
cgggcgcacc agtcgtagta atcccccaa accaaaggga a	401

<210> 278

<211> 401
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 278
 aatgagtgtg agaccacaaa tgaatgcccg gaggatgaaa tgtgttggaa ttatcatggc 60
 ggcttccgtt gttatccacg aaatccttgt caagatccct acattctaac accagagaac 120
 cgatgtgttt gccagtcctc aaatgccatg tgccgagAAC tgccccagtc aatagtctac 180
 aaatacatga gcatccgacg tgataggtct gtgccatcag acatcttcca gatacaggcc 240
 acaactattt atgccaacac catcaatact ttccggatta aatctggaaa tgaaaatgga 300
 gagtctacct acgacaacaa anccctgtaa gtgcaatgct tgtgctcgtg aagncattat 360
 caggaccaag agaacatatc gtggacctgg agatgctgac a 401

<210> 279
 <211> 401
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 279
 aaattattgc ctctgataca tacctaagtn aacanaacat taatacctaa gtaaacataa 60
 cattacttgg aggggttgag nttctaantg aaactgtatt tgaaactttt aagtatactt 120
 taggaacaaa gcatgaacgg cagtctagaa taccagaaac atctacttgg gtagcttggg 180
 gccattatcc tgtggaatct gatatgtctg gnagcatgct attgatggga catgaagaca 240
 tctttggaaa tgatgagatt atttcctgtg ttaaaaaaaaa aaaaaatctt aaattcctac 300
 aatgtgaaac tgaaactaat aattttgatc ctgatgtatg ggacagcgta tctgtaccag 360
 gctctaaata acaaaagnta gggngacaag nacatgttcc t 401

<210> 280
 <211> 326
 <212> DNA
 <213> Homo sapien

<400> 280
 gaagtggaaat tgtataattc aattcgataa ttgatctcat gggttttccc tggaggaaaag 60
 gttttttttg ttgttttttt ttttaagaact tgaaacttgt aaactgagat gtctgtagct 120
 tttttgcca tctgtagtgt atgtgaagat ttcaaaacct gagagcactt tttctttgtt 180
 tagaattatg agaaaggcac tagatgactt taggatttgc atttttccct ttattgcctc 240
 atttcttggt acgccttggt ggggagggaa atctgtttat tttttcctac aaataaaaaag 300
 ctaagattct atatcgcaaa aaaaaa 326

<210> 281
 <211> 374
 <212> DNA
 <213> Homo sapien

<400> 281
caacgcggttt gcaaataattc ccctggtagc ctacttccctt acccccgaat attggtgaaga 60
tcgagcaatg gcttcaggac atgggttctc ttctcctgtg atcattcaag tgctcactgc 120
atgaagactg gcttgtctca gtgtttcaac ctcaccaggg ctgtctcttg gtccacacct 180
cgctccctgt tagtgccgta tgacagcccc catcaaatga ccttggccaa gtcacggttt 240
ctctgtggtc aagggttggtt ggctgattgg tggaaagtag ggtggaccaa aggaggccac 300
gtgagcagtc agcaccagtt ctgcaccagc agcgcctccg tcctagtggg tgttccctgtt 360
tctcctggcc ctgg 374

<210> 282
<211> 404
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

<400> 282
agtgtggtgg aattccccgca tcctannccg cgactcacac aaggcagagt ngccatggag 60
aaaattccag tgtcagcatt cttgtctcctt gtggccctct cctacactct ggccagagat 120
accacagtca aacctgnagc caaaaaggac acaaaggact ctcgacccaa actgccccan 180
accctctcca gaggttgggg tgaccaactc atctggactc anacatatga agaagctcta 240
tataaatcca agacaagcaa caaaccttgg atgattattc atcacttgga tgagtgccca 300
cacagtcaag ctttaaagaa agtgtttgct gaaaataaag aaatccagaa attggcagag 360
cagtttgtcc tcctcaatct ggtttatgaa acaactgaca aaca 404

<210> 283
<211> 184
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(184)
<223> n = A,T,C or G

<400> 283
agtgtggtgg aattcacttg cttaanttgt gggcaaaaga gaaaaagaag gattgatcag 60
agcattgtgc aatacagttt cattaactcc ttccctcgct ccccaaaaaa ttgaatttt 120
tttttcaaca ctcttacacc tgttatggaa aatgtcaacc tttgtaagaa aaccaaata 180
aaaa 184

<210> 284
<211> 421
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = A,T,C or G

<400> 284

```

ctattaatcc tgccacaata tttttaatta cgtacaaaga tctgacatgt caccagggga      60
cccatttcac ccaactgctct gtttggecgc cagtcttttg tctctctctt cagcaatggg      120
gaggcgata ccctttcctc ggggaanana aatccatggg ttgttgccct tgccaataac      180
aaaaatggtg gaaagtcgag tggcaaagct gttgccattg gcattcttca cgtgaaccac      240
gtcaaaagat ccagggtgcc tctctctggt ggtgatcaca ccaattcttc ctaggttagc      300
acctccagtc accatacaca ggttaccagt gtcgaacttg atgaaatcag taatcttgcc      360
agtctctaaa tcaatctgaa tggatcatt caccttgatg aggggatcgg ggtagcggat      420
g                                           421

```

```

<210> 285
<211> 361
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(361)
<223> n = A,T,C or G

```

```

<400> 285
ctgggtggta actctttatt tcattgtccg gaanaaagat gggagtggga acagggtgga      60
cactgtgcag gcttcagctt ccactccggg caggattcag gctatctggg accgcaggga      120
ctgccagggtg cacagccctg gctcccaggg caggcaggca aggtgacggg actggaagcc      180
cttttcanag ccttgaggga gctggtccgt ccacaagcaa tgagtgccac tctgcagttt      240
gcaggggatg gataaacagg gaaacactgt gcattcctca cagccaacag ttaggtcctt      300
ggtgaagccc cggcgctgag ctaagctcag gctgttccag ggagccacga aactgcaggt      360
a                                           361

```

```

<210> 286
<211> 336
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(336)
<223> n = A,T,C or G

```

```

<400> 286
tttgagtggc agcgccctta tttgtggggg ccttcaaggg agggtcgtgg ggggcagcgg      60
ggaggaanag ccganaaact gtgtgaccgg ggcctcaggt ggtgggcatt gggggctcct      120
cttgcanatg ccatttgga tcaccgggtg agccattggg ggcagcgggt accggtcctt      180
tcttgttcaa catagggtag gtggcagcca cgggtccaac tcgcttgagg ctgggccctg      240
ggcgctccat tttgtgttcc angagcatgt ggttctgtgg cgggagcccc acgcaggccc      300
tgaggatggt ctcgatgcag ctgcgtgggc ggaaaaa                                336

```

```

<210> 287
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

<400> 287
 tgggtaccaaa atttntttat ttgaaggaat ggnacaaatc aaanaactta agnggatgtt 60
 ttggtacaac ttatanaaaa ggnaaaggaa accccaacat gcatgcnctg ccttgngac 120
 caggaagtc accccacggc tatggggaaa ttancccgag gcttancttt cattatcact 180
 gtctcccagg gngngcttgt caaaaanata ttccnccaag ccaaattcgg gcgctcccat 240
 nttgcncaag ttggtcacgt ggtcacccaa ttctttgatg gctttcacct gctcattcag 300
 g 301

<210> 288
 <211> 358
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (358)
 <223> n = A,T,C or G

<400> 288
 aagtttttaa actttttatt tgcatattaa aaaaattgng cattccaata attaaaatca 60
 tttgaacaaa aaaaaaaatg gcactctgat taaactgcat tacagcctgc aggacacctt 120
 gggccagctt gggttttactc tanatttcac tgcgtccca cccacttct tccacccac 180
 ttcttccttc accaacatgc aagttctttc cttccctgcc agccanata atagacagat 240
 gggaaaggca ggcgcggcct tcgttgtcag tagttctttg atgtgaaagg ggcagcacag 300
 tcatttaaac ttgatccaac ctctttgcat cttacaaagt taaacagcta aaagaagt 358

<210> 289
 <211> 462
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (462)
 <223> n = A,T,C or G

<400> 289
 ggcacagaa atgctgttta tttctctgct gctcccaagc tggctggcct ttgcagagga 60
 gcagacaaca gatgcatagt tgggganaaa gggaggacag gttccaggat agagggtgca 120
 ggctgaggga ggaagggtaa naggaaggaa ggccatcctg gatccccaca tttcagtctc 180
 anatgaggac aaagggactc ccaagcccc aaatcatcan aaaacaccaa ggagcaggag 240
 gagcttgagc aggccccagg gagcctcana gccataccag ccactgtcta cttcccatec 300
 tcctctccca ttccctgtct gcttcanacc acctcccagc taagccccag ctccattccc 360
 ccaatcctgg cccttgccag cttgacagtc acagtgcctg gaattccacc actgaggctt 420
 ctcccagttg gattaggacg tcgccctgtt agcatgctgc cc 462

<210> 290
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (481)

<223> n = A,T,C or G

<400> 290

tactttccta	aacttttatta	aagaaaaaag	caataagcaa	tggnggtaaa	tctctanaac	60
ataccecaatt	ttctgggctt	cctccccga	gaatgtgaca	ttttgatttc	caaacatgcc	120
anaagtgtat	ggttcccaac	tgtactaaag	taggtganaa	gctgaagtcc	tcaagtgttc	180
atcttccaac	ttttcccgat	ctgtggtctg	tctttggatc	agcaataatt	gcctgaacag	240
ctactatggc	ttcgttgatt	tttgtctgta	gctctctgag	ctcctctatg	tgcagcaatc	300
gcanaatttg	agcagcttca	ttaanaactg	catctcctgt	gtcaaaaacca	anaatatgtt	360
tgtctaaagc	aacaggtaag	ccctcttttg	tttgatttgc	cttancaact	gcacccctgtg	420
tcaggcgctc	ctgaacccaa	atccgaattg	ccttaagcat	taccaggtaa	tcacatgatc	480
g						481

<210> 291

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(381)

<223> n = A,T,C or G

<400> 291

tcataagtaat	gtaaaaccat	ttgtttaatt	ctaaatcaaa	tcactttcac	aacagtgaag	60
attagtgtact	gggttaaggng	tgccactgta	catatcatca	ttttctgact	ggggtcagga	120
cctgggtccta	gtccacaagg	gtggcaggag	gaggggtggag	gctaanaaca	cagaaaacac	180
acaaaanaaaa	ggaaagctgc	cttggcanaa	ggatgaggng	gtgagcttgc	cgaaggatgg	240
tgggaagggg	gctccctggt	ggggccgagc	caggagtccc	aagtcagctc	tcctgcctta	300
cttagctcct	ggcanagggt	gagtggggac	ctacgagggt	caaaatcaaa	tggcatttgg	360
ccagcctggc	tttactaaca	g				381

<210> 292

<211> 371

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(371)

<223> n = A,T,C or G

<400> 292

gaaaaaataa	tcogtttaat	tgaaaaacct	gnaggatact	attccactcc	cccanatgag	60
gaggctgagg	anaccaaacc	cctacatcac	ctcgtagcca	cttctgatac	tcttcacgag	120
gcagcaggca	aagacaattc	ccaaaacctc	nacaaaagca	attccaaggg	ctgctgcagc	180
taccaccanc	acatttttcc	tcagccagcc	cccaatcttc	tccacacagc	cctccttatg	240
gategccttc	tcgttgaaat	taatcccaca	gcccacagta	acattaatgc	ancaggagtc	300
ggggactcgg	ttcttcgaca	tggaagggat	tttctcccaa	tctgtgtagt	tagcagcccc	360
acagcactta	a					371

<210> 293

<211> 361

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (361)
<223> n = A,T,C or G

<400> 293
gattttaaag aaaacacttt attgttcagc aattaaaagt tagccaaata tgtatttttc 60
tccataattt attgngatgt tatcaacatc aagtaaaatg ctcatthttca tcatttgctt 120
ctgttcattgt tttcttgaac acgtcttcaa ttttcttcc aaaatgctgc atgccacact 180
tgaggtaacg aagcanaagt atttttaaac atgacagcta anaacattca tctacagcaa 240
cctatatgct caatacatgc cgcgtgatcc tagtagtttt ttcacaacct tctacaagtt 300
tttgaaaac atctgttatg atgactttca tacaccttca cctcaaaggc tttcttgcac 360
c 361

<210> 294
<211> 391
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (391)
<223> n = A,T,C or G

<400> 294
tattttaaag ttttaattatg attcanaaaa aatcgagcga ataactttct ctgaaaaaat 60
atattgactc tgtatanacc acagttattg gggganaagg gctggtaggt taaattatcc 120
tattttttat tctgaaaatg atattaatan aaagtcccgt ttccagtctg attataaaga 180
tacatatgcc caaaatggct ganaataaat acaacaggaa atgcaaaaagc tgtaaagcta 240
agggcatgca ananaaaatc tcanaatacc caaagnggca acaaggaacg tttggctgga 300
atttgaagtt atttcagtca tctttgtctt tggtccatg tttcaggatg cgtgtgaact 360
cgatgtaatt gaaattcccc tttttatcaa t 391

<210> 295
<211> 343
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (343)
<223> n = A,T,C or G

<400> 295
ttcttttgtt ttattgataa cagaaactgt gcataattac agatttgatg aggaatctgc 60
aaataataaa gaatgtgtct actgccagca aaatacaatt attccatgcc ctctcaacat 120
acaaatatag agttcttcac accanatggc tctggtgtaa caaagccatt ttanatgttt 180
aattgtgctt ctacaaaacc ttcanagcat gaggtagttt cttttacctt cnatattttc 240
cacatttcca ttattacact tttagttagc taaaatcctt ttaacatagc ctgcggatga 300
tctttcacaa aagccaagcc tcatttacia aggggtttatt tct 343

<210> 296
<211> 241
<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(241)

<223> n = A,T,C or G

<400> 296

ttcttgata ttggttgttt ttgtgaaaaa gtttttgttt ttcttctcag tcaactgaat	60
tatttctcta ctttgccctc ctgatgcca catgananaa cttaanataa tttctaacag	120
cttccacttt ggaaaaaaa aaaacctgtt ttctcatgg aacccagga gttgaaagt	180
gatanatcgc tctcaaaatc taaggctctg ttcagcttta cattatgta cctgacgttt	240
t	241

<210> 297

<211> 391

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(391)

<223> n = A,T,C or G

<400> 297

gttggtgctg anaatgctgg agatgctcag ttctctccct cacaaggtag gccacaaatt	60
cttggtggtg ccctcacatc tgggtcttc aggcaccagc catgcctgcc gaggagtgt	120
gtcaggacan accatgtccg tgctaggccc aggcacagcc caaccactcc tcatccaagt	180
ctctcccagg ttctctggtcc cgatgggcaa ggatgacccc tccagtggct ggtacccac	240
catcccacta cccctcacat gctctcactc tccatcaggt ccccaatcct ggcttccctc	300
ttcacgaact ctcaaagaaa aggaaggata aaacctaaat aaaccagaca gaagcagctc	360
tgaaaaagta caaaaagaca gccagaggtg t	391

<210> 298

<211> 321

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(321)

<223> n = A,T,C or G

<400> 298

caagccaaac tgnntccagc tttattaaan atactttcca taaacaatca tggattttca	60
ggcaggacat gggcanacaa tcgttaacag tatacaacaa ctttcaaact cccttnttca	120
atggactacc aaaaatcaaa aagccactat aaaacccaat gaagtcttca tctgatgtc	180
tgaacaggga aagtttaaag ngaggggtga catttcacat ttagcatgtt gtttaacaac	240
ttttcacaag ccgaccctga ctttcaggaa gtgaaatgaa aatggcanaa tttatctgaa	300
natccacaat ctaaaaatgg a	321

<210> 299

<211> 401

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 299
 tatcataaag agtggtgaag tttatattt atagcaccat tgagacattt tgaaattgga 60
 attggtaaaa aaataaaaaca aaaagcattt gaattgtatt tggnggaaca gcaaaaaaag 120
 agaagtatca tttttctttg tcaaattata ctgtttccaa acatttttga aataaataac 180
 tggaattttg tcggtcactt gcaactggtt acaagattag aacaagagga acacatatgg 240
 agttaaattt tttttgttgg gatttcanat agagtttggg ttataaaaag caaacagggc 300
 caacgtccac accaaattct tgatcaggac caccaatgtc atagggngca atatctacaa 360
 taggtagtct cacagccttg cgtgttcgat attcaaagac t 401

<210> 300
 <211> 188
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(188)
 <223> n = A,T,C or G

<400> 300
 tgaatgcttt gtcataattaa gaaagttaaa gtgcaataat gtttgaanac aataagtggg 60
 ggtgtatctt gtttctaata agataaactt ttttgtcttt gctttatctt attagggagt 120
 tgtatgtcag tgtataaaac atactgtgtg gtataacagg cttataaaat tctttaaaag 180
 gaaaaaaa 188

<210> 301
 <211> 291
 <212> DNA
 <213> Homo sapien

<400> 301
 aagattttgt tttatattt tatggctaga aagacactgt tatagccaaa atcggcaatg 60
 aactaaaga aatcctctgt gcttttcaat atgcaaata atttcttcca agagttgccc 120
 tgggtgtgact tcaagagttc atgttaactt cttttctgga aacttccttt tcttagttgt 180
 tgtattcttg aagagcctgg gccatgaaga gcttgcctaa gttttgggca gtgaactcct 240
 tgatgttctg gcagtaagtg tttatctggc ctgcaatgag cagcgagtcc a 291

<210> 302
 <211> 341
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(341)
 <223> n = A,T,C or G

<400> 302
 tgatttttca taattttatt aaatnatcac tgggaaaact aatgggttcg gtatcacaca 60


```

attacactac aatctgatag gagtggtaaa accagccaat ggaatccagg taaagtacaa 120
aaacgccacc ttttattgtc ctgtcttatt tctcggaag gagggttcta ctttacacat 180
ttcatgagcc agcagtggaac ttgagttaca atgtgtaggt tccttgtggt tatagtctga 240
gaagaagcca tcaaattctt gaggacttga catctctcgg aaagaagcaa actagtggat 300
cccccggtgc gcaggaattc gatatcaagc ttatcgatac c 341

```

```

<210> 303
<211> 361
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(361)
<223> n = A,T,C or G

```

```

<400> 303
tgcagacagt aaatnaattt tatttnggtt cacagaacat actaggcgat ctcgacagtc 60
gctccgtgac agccaccaa cccccaaccc tntacctcgc agccacccta aaggcgactt 120
caanaanatg gaaggatctc acggatctca ttctaatgg tccgccgaag tctcacacag 180
tanacagacg gagttganat gctggaggat gcagtcacct cctaaactta cgaccaccca 240
ccanacttca tcccagccgg gacgtcctcc cccaccggag tcttccccat ttcttctctc 300
actttgccgc agttccaggc gtctgtcttc caccagtccc acaaagctca ataaatacca 360
a 361

```

```

<210> 304
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 304
ctctttacaa cagcctttat ttncggccct tgatcctgct cggatgctgg tggaggccct 60
tagctccgcc cgccaggctc tgtgccgect ccccgaggc gcanattcat gaacacggtg 120
ctcaggggct tgaggccgta ctccccagc gggagctggt cctccagggg ctccccctcg 180
aaggtcagcc anaacaggtc gtctgcaca cctccagcc cgctcacttg ctgcttcagg 240
tgggccacgg tctgcgtcag cgcacctcg taggtgctgc tgcggccctt gttattcctc 300
a 301

```

```

<210> 305
<211> 331
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(331)
<223> n = A,T,C or G

```

```

<400> 305
ganaggctag taacatcagt tttattgggt tgggngggca accatagcct ggctgggggn 60

```

ggggctggcc	ctcacaggtt	gttgagttcc	agcaggggtct	ggtccaaggt	ctggtgaatc	120
tcgacgttct	cctccttggc	actggccaag	gtctcttcta	ggtcatcgat	ggttttctcc	180
aactttgcc	canacctctc	ggcaaaactct	gctcgggtct	cancctcctt	cagcttctcc	240
tccaacagtt	tgatctctc	ttcatattta	tcttctttgg	gggaatactc	ctcctctgag	300
gccatcaggg	acttgagggc	ctggtccatg	g			331

<210> 306
 <211> 457
 <212> DNA
 <213> Homo sapien

<400> 306						
aatatgtaaa	ggtaataact	tttattatat	ttaaagacaat	gcaaacgaaa	aacagaattg	60
agcagtgcaa	aatttaaagg	actgttttgt	tctcaaagtt	gcaagtttca	aagccaaaag	120
aattatatgt	atcaaatata	taagtaaaaa	aaagttagac	tttcaagcct	gtaatcccag	180
cactttggga	ggctgaggca	ggtggatcac	taacattaaa	aagacaacat	tagattttgt	240
cgatttatag	caattttata	aatatataac	tttgtcactt	ggatcctgaa	gcaaaataat	300
aaagtgaatt	tgggattttt	gtacttggt	aaaagtttaa	caccctaaat	tcacaactag	360
tggatcccc	gggctgcagg	aattcgatat	caagcttatc	gataccgtcg	acctcgaggg	420
ggggcccggg	acccaattcg	ccctatagtg	agtcgta			457

<210> 307
 <211> 491
 <212> DNA
 <213> Homo sapien

<400> 307						
gtgcttgga	ggaacccggc	gctcgttccc	caccccgggc	ggcgcgccat	agccagccct	60
ccgtcacctc	ttcacgcac	cctcggactg	ccccaaaggc	cccgcgcgcg	ctccagcgcc	120
gcgcagccac	gcgcgcgcgc	gccgcctctc	cttagtcgcc	gccatgacga	ccgcgtccac	180
ctcgcaggtg	cgccagaact	accaccagga	ctcagaggcc	gccatcaacc	gccagatcaa	240
cctggagctc	tacgcctoct	acgtttacct	gtccatgtct	tactactttg	accgcgatga	300
tgtggctttg	aagaactttg	ccaaataactt	tcttcaccaa	tctcatgagg	agagggaaca	360
tgctgagaaa	ctgatgaagc	tgcagaacca	acgaggtggc	cgaatcttcc	ttcaggatat	420
caagaaacca	gactgtgatg	actgggagag	cgggctgaat	gcaatggagt	gtgcattaca	480
tttggaaaaa	a					491

<210> 308
 <211> 421
 <212> DNA
 <213> Homo sapien

<400> 308						
ctcagcgctt	cttctttctt	ggtttgatcc	tgactgctgt	catggcgtgc	cctctggaga	60
aggccctgga	tgtgatgggtg	tcacacttcc	acaagtactc	gggcaaagag	ggtgacaagt	120
tcaagctcaa	caagtcagaa	ctaaaggagc	tgctgacccg	ggagctgccc	agcttcttgg	180
ggaaaaggac	agatgaagct	gctttccaga	agctgatgag	caacttggac	agcaacaggg	240
acaacgaggt	ggacttccaa	gagtactgtg	tcttcctgtc	ctgcatcgcc	atgatgtgta	300
acgaattctt	tgaaggcttc	ccagataagc	agcccaggaa	gaaatgaaaa	ctcctctgat	360
gtgggtgggg	ggtctgccag	ctggggccct	ccctgtcgcc	agtgggcact	tttttttttc	420
c						421

<210> 309
 <211> 321
 <212> DNA

<213> Homo sapien

<400> 309

accaaattggc	ggatgacgcc	ggtgcagcgg	ggggggcccg	gggccctggg	ggccctggga	60
tggggaaccg	cgggtggcttc	cgcgagaggt	tcggcagtg	catccggggc	cggggtcgcg	120
gccgtggacg	gggccggggc	cgaggccgcg	gagctcgcg	aggcaaggcc	gaggataagg	180
agtggatgcc	cgtcaccaag	ttgggccgct	tggccaagga	catgaagatc	aagtccttgg	240
aggagatcta	tctcttctcc	ctgccatta	aggaatcaga	gatcattgat	ttcttcctgg	300
gggcctctct	caaggatgag	g				321

<210> 310

<211> 381

<212> DNA

<213> Homo sapien

<400> 310

ttaaccagcc	atattggctc	aataaatagc	ttcggtaagg	agttaatttc	cttctagaaa	60
tcagtgccta	tttttcctgg	aaactcaatt	ttaaatagtc	caattccatc	tgaagccaag	120
ctgttgtcat	tttcattcgg	tgacattctc	tcctatgaca	cccagaagg	gcagaagaac	180
cacatttttc	atttatagat	gtttgcatcc	tttgtattaa	aattattttg	aaggggttgc	240
ctcattggat	ggcttttttt	tttttcctcc	agggagaagg	ggagaaatgt	acttggaat	300
taatgtatgt	ttacatctct	ttgcaaattc	ctgtacatag	agatatattt	tttaagtgtg	360
aatgtaacaa	catactgtga	a				381

<210> 311

<211> 538

<212> DNA

<213> Homo sapien

<400> 311

tttgaattta	caccaagaac	ttctcaataa	aagaaaatca	tgaatgctcc	acaatttcaa	60
cataccacaa	gagaagttaa	tttcttaaca	tttgtttcta	tgattatttg	taagaccttc	120
accaagttct	gatatctttt	aaagacatag	ttcaaaattg	cttttgaaaa	tctgtattct	180
tgaataatc	cttgttgtgt	attaggtttt	taaataccag	ctaaaggatt	acctcactga	240
gtcatcagta	ccctcctatt	cagctcccca	agatgatgtg	tttttgctta	ccctaagaga	300
ggtttttctc	ttatttttag	ataattcaag	tgcttagata	aattatgttt	tctttaagtg	360
tttatggtaa	actcttttaa	agaaaattta	atatgttata	gctgaatctt	tttggttaact	420
ttaaatcttt	atcatagact	ctgtacatat	gttcaaatta	gctgcttgcc	tgatgtgtgt	480
atcatcgggtg	ggatgacaga	acaaacatat	ttatgatcat	gaataatgtg	ctttgttaa	538

<210> 312

<211> 176

<212> DNA

<213> Homo sapien

<400> 312

ggaggagcag	ctgagagata	gggtcagtga	atgcggttca	gcctgctacc	tctcctgtct	60
tcatagaacc	attgccttag	aattattgta	tgacacgttt	tttgttggtt	aagctgtaag	120
gttttggtct	ttgtgaacat	gggtattttg	aggggagggg	ggaggagta	gggaag	176

<210> 313

<211> 396

<212> DNA

<213> Homo sapien

<400> 313

ccagcacc	cc	caggccctgg	gggacctggg	ttctcagact	gccaaagaag	ccttgccatc	60
tggcgctccc	at	ggctcttg	caacatctcc	ccttcgtttt	tgaggggggtc	atgccggggg	120
agccaccagc	cc	ctcactgg	gttcggagga	gagtcaggaa	gggccaagca	cgacaaagca	180
gaaacatcgg	at	ttggggaa	cgcgtgtcaa	tcccttgtgc	cgcaggggctg	ggcgggagag	240
actgtttctgt	tc	cttgtgta	actgtgttgc	tgaaagacta	cctcgttctt	gtcttgatgt	300
gtcaccgggg	ca	actgcctg	ggggcgggga	tgggggcagg	gtggaagcgg	ctccccattt	360
tataccaaag	gt	gctacatc	tatgtgatgg	gtgggg			396

<210> 314

<211> 311

<212> DNA

<213> Homo sapien

<400> 314

cctcaacatc	ct	cagagagg	actggaagcc	agtccttacg	ataaactcca	taatttatgg	60
cctgcagtat	ct	cttcttgg	agcccaaccc	cgaggaccca	ctgaacaagg	aggccgcaga	120
ggctctgcag	aa	caaccggc	ggctgtttga	gcagaacgtg	cagcgctcca	tgcgggggtg	180
ctacatcggc	tc	cacctact	ttgagcgctg	cctgaaatag	ggttggcgca	taccaccccc	240
cgccacggcc	aa	agccctg	gcatcccctg	caaatattta	ttggggggcca	tgggtagggg	300
tttggggggc	g						311

<210> 315

<211> 336

<212> DNA

<213> Homo sapien

<400> 315

tttagaacat	gg	ttatcatc	caagactact	ctaccctgca	acattgaact	cccaagagca	60
aatccacatt	c	ctcttgagt	tctgcagctt	ctgtgtaaat	agggcagctg	tcgtctatgc	120
cgtagaatca	cat	gatctga	ggaccattca	tggaaagctgc	taaatagcct	agtctgggga	180
gtcttccata	aa	gtttttgca	tggagcaaac	aaacaggatt	aaactagggt	tggttccttc	240
agccctctaa	aa	gcataggg	cttagcctgc	aggcttcctt	gggctttctc	tgtgtgtgta	300
gttttgtaaa	c	actatagca	tctgttaaga	tccagt			336

<210> 316

<211> 436

<212> DNA

<213> Homo sapien

<400> 316

aacatggctc	gc	gtgcctta	agagagacgc	ttcctgcaga	acaggacctg	actacaaaga	60
atgtttccat	tg	gaattggt	ggtaaagact	tggagtttac	aatctatgat	gatgatgatg	120
tgtctccatt	c	ctggaagg	cttgaagaaa	gaccacagag	aaaggcacag	cctgctcaac	180
ctgctgatga	ac	ctgcagaa	aaggctgatg	aaccaatgga	acattaagtg	ataagccagt	240
ctatatatgt	att	atcaaat	atgtaagaat	acaggcacca	catactgatg	acaataatct	300
atactttgaa	cc	aaaagttg	cagagtgggtg	gaatgctatg	ttttaggaat	cagtcagat	360
gtgagttttt	tc	caagcaac	ctcactgaaa	cctatatataat	ggaatacatt	tttctttgaa	420
agggctctgta	ta	atca					436

<210> 317

<211> 196

<212> DNA

<213> Homo sapien

<400> 317

tattccttgt	gaagatgata	tactatTTTT	gttaagcgtg	tctgtattta	tgtgtgagga	60
gctgctggct	tgcagtgcgc	gtgcacgtgg	agagctgggtg	cccggagatt	ggacggcctg	120
atgctccctc	ccctgccttg	gtccagggaa	gctggccgag	ggctcctggct	cctgaggggc	180
atctgccctc	ccccca					196

<210> 318

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (381)

<223> n = A,T,C or G

<400> 318

gacgcttnng	ccgtaacgat	gatcggagac	atcctgctgt	tcgggacgtt	gctgatgaat	60
gccggggcgg	tgctgaactt	taagctgaaa	aagaaggaca	cncagggtt	tggggaggag	120
tncagggagc	ccaacacagg	tgacaacatc	cgggaattct	tgctgancct	cagatacttt	180
cnaatcttca	tcnccctgtg	gaacatcttc	atgatgttct	gcatgattgt	gctgntcggc	240
tcttgaatcc	cancgatgaa	accannaact	cactttcccg	ggatgccgan	tctccattcc	300
tccattcctg	atgacttcaa	naatgttttt	gaccaaaaaa	ccgacaacct	tcccagaaag	360
tccaagctcg	tggtggngg	a				381

<210> 319

<211> 506

<212> DNA

<213> Homo sapien

<400> 319

ctaagcttta	cgaatggggt	gacaacttat	gataaaaact	agagctagt	aattagccta	60
tttgtaaata	cctttgttat	aattgatagg	atacatcttg	gacatggaat	tgttaagcca	120
cctctgagca	gtgtatgtca	ggacttggtc	attaggttgg	cagcagagg	gcagaaggaa	180
ttatacaggt	agagatgtat	gcagatgtgt	ccatatatgt	ccatatttac	atthttgatag	240
ccattgatgt	atgcatctct	tggctgtact	ataagaacac	attaattcaa	tggaaatata	300
ctttgcta	atthttaatg	tatagatctg	ctaatagaat	ctcttaaaaa	catactgtat	360
tctgttgctg	tgtgtttcat	tttaaatga	gcattaagg	aatgcagcat	ttaaatcaga	420
actctgccaa	tgcttttatc	tagaggcgtg	ttgccatttt	tgtcttatat	gaaattttctg	480
tcccaagaaa	ggcaggatta	catctt				506

<210> 320

<211> 351

<212> DNA

<213> Homo sapien

<400> 320

ctgacctgca	ggacgaaacc	atgaagagcc	tgatccttct	tgccatcctg	gccgccttag	60
cggtagtaac	tttgtgttat	gaatcacatg	aaagcatgga	atcttatgaa	cttaatccct	120
tcattaacag	gagaaatgca	aataccttca	tatccccctca	gcagagatgg	agagctaaag	180
tccaagagag	gatccgagaa	cgctctaagc	ctgtccacga	gctcaatagg	gaagcctgtg	240
atgactacag	actttgcgaa	cgctacgcca	tggtttatgg	atacaatgct	gcctataatc	300
gctacttcag	gaagcgccga	gggaccaa	gagactgagg	gaagaaaaaa	a	351

<210> 321

<211> 421
 <212> DNA
 <213> Homo sapien

<400> 321
 ctccggaggcg ttcagctgct tcaagatgaa gctgaacatc tccttcccag ccactggctg 60
 ccagaaaactc attgaagtgg acgatgaacg caaacttcgt actttctatg agaagcgtat 120
 ggccacagaa gttgctgctg acgctctggg tgaagaatgg aagggttatg tgggccgaat 180
 cagtgggtggg aacgacaaac aagggtttccc catgaagcag ggtgtcttga cccatggccg 240
 tgtccgcctg ctactgagta aggggcattc ctgttacaga ccaaggagaa ctggagaaaag 300
 aaagagaaaa tcagttcgtg gttgcattgt ggatgcaaat ctgagcgttc tcaacttggg 360
 tattgtaaaa aaaggagaga aggatattcc tggactgact gatactacag tgcctcgccg 420
 c 421

<210> 322
 <211> 521
 <212> DNA
 <213> Homo sapien

<400> 322
 agcagctctc ctgccacagc tcctcacccc ctgaaaatgt tcgcctgctc caagtttgtc 60
 tccactccct ccttgggtcaa gagcacctca cagctgctga gccgtccgct atctgcagtg 120
 gtgctgaaac gaccggagat actgacagat gagagcctca gcagcttggc agtctcatgt 180
 ccccttacct cacttgtctc tagccgcagc ttccaaacca gcgccatttc aagggacatc 240
 gacacagcag ccaagttcat tggagctggg gctgccacag ttgggggtggc tggttctggg 300
 gctgggattg gaactgtgtt tgggagcctc atcattgggt atgccaggaa cccttctctg 360
 aagcaacagc tcttctccta cgccattctg ggctttgccc tctcggaggc catggggctc 420
 ttttgtctga tggtagcctt tctcatcctc tttgccatgt gaaggagccg tctccacctc 480
 ccatagttct cccgcgtctg gttggccccg tgtgttcctt t 521

<210> 323
 <211> 435
 <212> DNA
 <213> Homo sapien

<400> 323
 ccgaggtcgc acgcgtgaga cttctccgcc gcagacgccg ccgcgatgcg ctacgtcgcc 60
 tctacactgc tggctgccct agggggcaac tcctccccca gcgccaagga catcaagaag 120
 atcttggaac gcgtgggtat cgaggcggac gacgaccggc tcaacaaggt tatcagtga 180
 ctgaatggaa aaaacattga agacgtcatt gccagggtta ttggcaagct tgccagtga 240
 cctgctgggt gggctgtagc cgtctctgct gcccagggt ctgcagcccc tgctgctggt 300
 tctgccccctg ctgcagcaga ggagaagaaa gatgagaaga aggaggagtc tgaagagtca 360
 gatgatgaca tgggatttgg cctttttgat taaattcctg ctccctgca aataaagcct 420
 ttttacacat ctcaa 435

<210> 324
 <211> 521
 <212> DNA
 <213> Homo sapien

<400> 324
 aggagatcga ctttcggtgc ccgcaagacc agggctggaa cgccgagatc acgctgcaga 60
 tgggtgcagta caagaatcgt caggccatcc tggcgggtcaa atccacgcgg cagaagcagc 120
 agcacctggt ccagcagcag cccccctcgc agccgcagcc gcagccgcag ctccagcccc 180
 aacccccagcc tcagcctcag ccgcaacccc agccccaatc acaaccccag cctcagcccc 240

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aaccacaagcc tcagcccccag cagctccacc cgtatccgca tccacatcca catccacact 300
ctcctcctca ctgcgaccca caccctcacc cgcacccgca tccgcacca ataccgcacc 360
cacacccaca gccgcactcg cagccgcacg ggcaccgget tctccgcagc acctccaact 420
ctgcctgaaa ggggcagctc ccgggcaaga caagggtttg aggacttgag gaagtgggac 480
gagcacattt ctattgtctt cacttggatc aaaagcaaaa c 521

```

<210> 325

<211> 451

<212> DNA

<213> Homo sapien

<400> 325

```

attttcattt ccattaacct ggaagctttc atgaatatcc tcttctttta aaacatttta 60
acattattta aacagaaaaa gatgggctct ttctggtag ttgttacatg atagcagaga 120
tatttttact tagattactt tgggaatgag agattgttgt cttgaactct ggcactgtac 180
agtgaatgtg tctgtagtgt tgtagtttg cattaagcat gtataacatt caagtatgtc 240
atccaaataa gaggcataata cattgaattg tttttaatcc tctgacaagt tgactcttcg 300
acccccaccc ccaccaaga cattttaata gtaaatagag agagagagaa gagttaatga 360
acatgaggtg gtgttcact ggcaggatga cttttcaata gctcaaatca atttcagtgc 420
ctttatcact tgaattatta acttaatttg a 451

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<210> 326

<211> 421

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(421)

<223> n = A,T,C or G

<400> 326

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cgcggtcgta agggctgagg atttttggtc cgcacgctcc tgctcctgac tcaccgctgt 60
tcgctctcgc cgaggaacaa gtcggtcagg aagcccgccg gcaacagcca tggcttttaa 120
ggataccgga aaaacacccg tggagccgga ggtggcaatt caccgaattc gaatcaccct 180
aacaagccgc aacgtaaaat ccttggaaaa ggtgtgtgct gacttgataa gaggcgcaaa 240
agaaaagaat ctcaaagtga aaggaccagt tcgaatgcct accaagactt tgagantcac 300
tacaagaaaa actccttgtg gtgaagggtc taagacgtgg gatcgtttcc agatgagaat 360
tcacaagcga ctcattgact tgcacagctc ttctgagatt gttaagcaga ttacttccat 420
c 421

```

<210> 327

<211> 456

<212> DNA

<213> Homo sapien

<400> 327

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atcttgacga ggctgcggtg tctgctgcta ttctccgagc ttcgcaatgc cgcctaagga 60
cgacaagaag aagaaggacg ctggaaagtc ggccaagaaa gacaaagacc cagtgaacaa 120
atccgggggc aaggccaaaa agaagaagtg gtccaaaggc aaagtccggg acaagctcaa 180
taacttagtc ttgtttgaca aagctacctg tgataaactc tgtaaggaag ttcccaacta 240
taaacttata accccagctg tggctctctg gagactgaag attcgaggct ccctggccag 300
ggcagccctt caggagctcc ttagtaaaag acttatcaaa ctggtttcaa agcacagagc 360
tcaagtaatt tacaccagaa ataccaaggg tggagatgct ccagctgctg gtgaagatgc 420
atgaataggt ccaaccagct gtacatttgg aaaaat 456

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<210> 328
 <211> 471
 <212> DNA
 <213> Homo sapien

<400> 328
 gtggaagtga catcgtcttt aaaccctgcg tggcaatccc tgacgcaccg ccgtgatgcc 60
 caggaagac agggcgacct ggaagtccaa ctacttcctt aagatcatcc aactattgga 120
 tgattatccg aaatgtttca ttgtgggagc agacaatgtg ggctccaagc agatgcagca 180
 gatccgcatg tcccttcgcg ggaaggctgt ggtgctgatg ggcaagaaca ccatgatgcy 240
 oaaggccatc cgagggcacc tggaaaacaa cccagctctg gagaaactgc tgcctcatat 300
 cggggggaat gtgggctttg tgttcaccaa ggaggacctc actgagatca gggacatgtt 360
 gctggccaat aagggtgccag ctgctgcccg tgctggtgcc attgccccat gtgaagtcac 420
 tgtgccagcc cagaacactg gtctcgggccc cgagaagacc tcctttttcc a 471

<210> 329
 <211> 278
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (278)
 <223> n = A,T,C or G

<400> 329
 gtttaactt aagcttggtg cgcagctcgg atccactagt ccagtgtggt ggaattctag 60
 aaattgagat gccccccag gccagcaaat gttccttttt gttcaaagtc tatttttatt 120
 ccttgatatt tttctttttt tttttttttt ttnggatgg ggacttgtga atttttctaa 180
 aggtgctatt taacatggga gganagcgtg tgcggtcca gccagcccg ctgctcactt 240
 tccacctct ctcacctgc ctctggcttc tcaggcct 278

<210> 330
 <211> 338
 <212> DNA
 <213> Homo sapien

<400> 330
 ctcaggcttc aacatcgaat acgcgcgagg ccccttcgcc ctattcttca tagccgaata 60
 cacaaacatt attataataa acaccctcac cactacaatc ttctaggaa caacatatga 120
 cgcactctcc cctgaactct acacaacata ttttgtcacc aagaccctac ttctaacctc 180
 cctgttctta tgaattcgaa cagcataccc ccgattccgc tacgaccaac tcatacacct 240
 cctatgaaaa aacttctac cactcaccct agcattactt atatgatatg tctccatacc 300
 cattacaatc tccagcatte cccctcaaac ctaaaaaa 338

<210> 331
 <211> 2820
 <212> DNA
 <213> Homo sapiens

<400> 331
 tggcaaaatg ctggagccag aagaaaggac agcagcattg atcaatctta cagctaaccat 60
 gttgtacctg gaaaacaatg cccagactca atttagtgag ccacagtaca cgaacctggg 120


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gctcctgaac agcatggacc agcagattcg gaacggctcc tcgtccacca gtccctataa 180
cacagaccac gcgcagaaca gcgtcacggc gccctcgccc tacgcacagc ccagccccac 240
cttcgatgct ctctctccat cacccgccat cccctccaac accgactacc caggccccga 300
cagttccgac gtgtcccttc agcagtcgag caccgccaag tcggccacct ggacgtattc 360
cactgaactg aagaaactct actgccaaat tgcaaagaca tgcccatcc agatcaaggt 420
gatgacccca cctcctcagg gagctgttat ccgcgccatg cctgtctaca aaaaagctga 480
gcacgtcacg gaggtggtga agcgggtgcc caaccatgag ctgagccgtg agttcaacga 540
gggacagatt gccctccta gtcatttgat tcgagtagag gggaacagcc atgccagta 600
tgtagaagat cccatcacag gaagacagag tgtgtggtta ccttatgagc caccacaggt 660
tggcactgaa ttcacgacag tcttgtaaa tttcatgtgt aacagcagtt gtgttgagg 720
gatgaaccgc cgtccaattt taatcattgt tactctggaa accagagatg ggcaagtcct 780
gggcccagcg tgctttgagg cccggatctg tgcttgccca ggaagagaca ggaaggcgga 840
tgaagatagc atcagaaagc agcaagtttc ggacagtaca aagaacgggtg atggtacgaa 900
gcgcccgttt cgtcagaaca cacatggtat ccagatgaca tccatcaaga aacgaagatc 960
cccagatgat gaactgttat acttaccagt gaggggcccgt gagacttatg aaatgctgtt 1020
gaagatcaaa gagtccctgg aactcatgca gtaccttct cagcacacaa ttgaaacgta 1080
caggcaacag caacgacagc agcaccagca cttacttcag aaacagacct caatacagtc 1140
tccatcttca tatggttaaca gctccccacc tctgaacaaa atgaacagca tgaacaagct 1200
gccttctgtg agccagctta tcaaccctca gcagcgcaac gccctcactc ctacaaccat 1260
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<210> 332

<211> 2270

<212> DNA

<213> Homo sapiens

<400> 332

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<211> 2816

<212> DNA

<213> Homo sapiens

<400> 333

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<210> 334

<211> 2082

<212> DNA

<213> Homo sapiens

<400> 334

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<211> 4849

<212> DNA

<213> Homo sapiens

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<211> 1386

<212> DNA

<213> Homo sapiens

<400> 336

atgttggtacc tggaaaacaa tgcccagact caatttagtg agccacagta cacgaacctg 60
 gggctcctga acagcatgga ccagcagatt cagaacggct cctcgccac cagtccttat 120
 aacacagacc acgcgcagaa cagcgtcacg ggcgcctcgc cctacgcaca gccagctcc 180
 accttcgatg ctctctctcc atcaccgcc atccctcca acaccgacta cccagggccg 240
 cacagtttcg acgtgtcctt ccagcagtcg agcaccgcca agtcggccac ctggacgtat 300
 tccactgaac tgaagaaact ctactgccaa attgcaaaga catgccccat ccagatcaag 360
 gtgatgacct cacctcctca gggagctgtt atccgcgcca tgctgtcta caaaaaagct 420
 gagcacgtca cggagggtgg gaagcgtgac cccaaccatg agctgagccg tgaattcaac 480
 gaggggacaga ttgcccctcc tagtcatttg attcgagtag aggggaacag ccatgcccag 540
 tatgtagaag atcccatcac aggaagacag agtggtgctg taccttatga gccacccag 600
 gttggcactg aattcacgac agtcttgtag aatttcattgt gtaacagcag ttgtgttgga 660
 gggatgaacc gccgtccaat tttaatcatt gttactctgg aaaccagaga tgggcaagtc 720
 ctgggcccag gctgctttga ggcccggatc tgtgcttgcc caggaagaga caggaaggcg 780
 gatgaagata gcatcagaaa gcagcaagtt tgggacagta caaagaacgg tgatggtacg 840
 aagcgcgccgt ttcgtcagaa cacacatggt atccagatga catccatcaa gaaacgaaga 900
 tccccagatg atgaactggt atacttacca gtgagggggc gtgagactta tgaatgctg 960
 ttgaagatca aagagtccct ggaactcatg cagtaccttc ctcagcacac aattgaaacg 1020
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 attcctgatg gcatgggagc caacattccc atgatgggca cccacatgcc aatggctgga 1260
 gacatgaatg gactcagccc caccagggca ctccctcccc cactctccat gccatccacc 1320
 tcccactgca cccccccacc tccgtatccc acagattgca gcattgtcag gatctggcaa 1380
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<210> 337

<211> 1551

<212> DNA

<213> Homo sapiens

<400> 337

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 gattttctgg aacagcctat atgttcagtt cagccattg acttgaactt tgtggatgaa 120
 ccatcagaag atggtgagc aaacaagatt gagattagca tggactgtat ccgcatgcag 180
 gactcggacc tgagtgacct catgtggcca cagtacagca acctggggct cctgaacagc 240
 atggaccagc agattcagaa cggctcctcg tccaccagtc cctataaac agaccacgcg 300
 cagaacagcg tcacggcgcc ctgcgcctac gcacagccca gctccacctt cgatgctctc 360
 tctccatcac ccgccatccc ctccaacacc gactaccag gcccgcacag tttcgacgtg 420
 tccttccagc agtcgagcac cgccaagtc gccacctgga cgtattccac tgaactgaag 480
 aaactctact gccaaattgc aaagacatgc cccatccaga tcaagggtgat gacccacct 540
 cctcaggag ctgttatccg cgccatgct gtctacaaaa aagctgagca cgtcacggag 600
 gtggtgaagc ggtgccccaa ccatgagctg agccgtgaat tcaacgaggg acagattgcc 660
 cctcctagtc atttgattcg agtagagggg aacagccatg cccagtatgt agaagatccc 720

```

atcacaggaa gacagagtgt gctggtacct tatgagccac cccaggttgg cactgaattc 780
acgacagtct tgtacaattt catgtgtaac agcagttgtg ttggagggat gaaccgccgt 840
ccaattttta tcattgttac tctggaaacc agagatgggc aagtcctggg ccgacgctgc 900
tttgaggccc ggatctgtgc ttgcccagga agagacagga aggcggatga agatagcatc 960
agaaagcagc aagtttcgga cagtacaaag aacggtgatg gtacgaagcg cccgtttcgt 1020
cagaacacac atggtatcca gatgacatcc atcaagaaac gaagatcccc agatgatgaa 1080
ctgtttatact taccagttag gggccgtgag acttatgaaa tgctgttgaa gatcaaagag 1140
tccctggaac tcatgcagta ccttcctcag cacacaattg aaacgtacag gcaacagcaa 1200
cagcagcagc accagcactt acttcagaaa cagacctcaa tacagtctcc atcttcatat 1260
ggtaacagct ccccacctct gaacaaaatg aacagcatga acaagctgcc ttctgtgagc 1320
cagcttatca accctcagca gcgcaacgcc ctcaactcta caaccattcc tgatggcatg 1380
ggagccaaca ttcccatgat gggcacccac atgccaatgg ctggagacat gaatggactc 1440
agccccaccc aggcactccc tccccactc tccatgccat ccacctccca ctgcacaccc 1500
ccacctccgt atccccacaga ttgcagcatt gtcaggatct ggcaagtctg a 1551

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<210> 338

<211> 586

<212> PRT

<213> Homo sapiens

<400> 338

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Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
      5                      10                      15

```

```

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Arg Asn
      20                      25                      30

```

```

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
      35                      40                      45

```

```

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Pro Thr Phe Asp Ala
      50                      55                      60

```

```

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
      65                      70                      75                      80

```

```

His Ser Ser Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
      85                      90                      95

```

```

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
      100                     105                     110

```

```

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
      115                     120                     125

```

```

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
      130                     135                     140

```

```

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
      145                     150                     155                     160

```

```

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
      165                     170                     175

```

```

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val

```

180	185	190
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val		
195	200	205
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg		
210	215	220
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val		
225	230	235
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg		
245	250	255
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp		
260	265	270
Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr		
275	280	285
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp		
290	295	300
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu		
305	310	315
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His		
325	330	335
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu		
340	345	350
Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser		
355	360	365
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val		
370	375	380
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr		
385	390	395
Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met		
405	410	415
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro		
420	425	430
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro		
435	440	445
Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys		
450	455	460
Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr		
465	470	475
		480

Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
485 490 495

Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
500 505 510

Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
515 520 525

Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
530 535 540

Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
545 550 555 560

Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
565 570 575

Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
580 585

<210> 339

<211> 641

<212> PRT

<213> Homo sapiens

<400> 339

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg

435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Gly
 500 505 510
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640
 Glu

<210> 340

<211> 448

<212> PRT

<213> Homo sapiens

<400> 340

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415

Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430

Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 341

<211> 356

<212> PRT

<213> Homo sapiens

<400> 341

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn

145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Ser Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln
 355
 <210> 342
 <211> 680
 <212> PRT
 <213> Homo sapiens
 <400> 342
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 5 10 15
 Pro Tyr Ile Gln Arg Phe Val Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30
 Glu Ser Tyr Tyr Arg Ser Thr Met Ser Gln Ser Thr Gln Thr Asn Glu
 35 40 45

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60
 Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro
 65 70 75 80
 Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95
 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110
 Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
 115 120 125
 Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr
 130 135 140
 Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser
 145 150 155 160
 Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser
 165 170 175
 Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp
 180 185 190
 Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr
 195 200 205
 Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val
 210 215 220
 Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val
 225 230 235 240
 Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly
 245 250 255
 Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His
 260 265 270
 Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val
 275 280 285
 Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr
 290 295 300
 Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro
 305 310 315 320
 Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly
 325 330 335

Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg
 340 345 350
 Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr
 355 360 365
 Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly
 370 375 380
 Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu
 385 390 395 400
 Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys
 405 410 415
 Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile
 420 425 430
 Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln
 435 440 445
 Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro
 450 455 460
 Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln
 465 470 475 480
 Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro
 485 490 495
 Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met
 500 505 510
 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro
 515 520 525
 Leu Ser Met Pro Ser Thr Ser Gln Cys Thr Pro Pro Pro Tyr Pro
 530 535 540
 Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser
 545 550 555 560
 Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile
 565 570 575
 Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln
 580 585 590
 Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
 595 600 605
 Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser
 610 615 620
 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp

625 630 635 640
 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp
 645 650 655
 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln
 660 665 670
 Gln Arg Ile Lys Glu Glu Gly Glu
 675 680

 <210> 343
 <211> 461
 <212> PRT
 <213> Homo sapiens

 <400> 343
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 450 455 460

<210> 344

<211> 516

<212> PRT

<213> Homo sapiens

<400> 344

290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Arg
 500 505 510
 Ile Trp Gln Val
 515

<210> 345

<211> 1800

<212> DNA

<213> Homo sapiens

<400> 345

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 actggttggtt ttttaaacaattctgatac aggcgacatc ctactgacc gagcaaagat 120
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<210> 346

<211> 261

<212> PRT

<213> Homo sapiens

<400> 346

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Ser Thr Ser Ile Gly Lys Val Trp Ile Thr Val Ile Phe Ile Phe Arg
20 25 30

Val Met Ile Leu Val Val Ala Ala Gln Glu Val Trp Gly Asp Glu Gln
35 40 45

Glu Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys
50 55 60

Tyr Asp His Phe Phe Pro Val Ser His Ile Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ala Leu Leu Val Ala Met His Val Ala
85 90 95

Tyr Tyr Arg His Glu Thr Thr Arg Lys Phe Arg Arg Gly Glu Lys Arg
100 105 110

Asn Asp Phe Lys Asp Ile Glu Asp Ile Lys Lys His Lys Val Arg Ile
 115 120 125
 Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Ile
 130 135 140
 Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Phe Leu Tyr Asn Gly
 145 150 155 160
 Tyr His Leu Pro Trp Val Leu Lys Cys Gly Ile Asp Pro Cys Pro Asn
 165 170 175
 Leu Val Asp Cys Phe Ile Ser Arg Pro Thr Glu Lys Thr Val Phe Thr
 180 185 190
 Ile Phe Met Ile Ser Ala Ser Val Ile Cys Met Leu Leu Asn Val Ala
 195 200 205
 Glu Leu Cys Tyr Leu Leu Leu Lys Val Cys Phe Arg Arg Ser Lys Arg
 210 215 220
 Ala Gln Thr Gln Lys Asn His Pro Asn His Ala Leu Lys Glu Ser Lys
 225 230 235 240
 Gln Asn Glu Met Asn Glu Leu Ile Ser Asp Ser Gly Gln Asn Ala Ile
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 Thr Gly Phe Pro Ser
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<210> 347

<211> 1740

<212> DNA

<213> Homo sapiens

<400> 347

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<210> 348
<211> 579
<212> PRT
<213> Homo sapiens
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<400> 348
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20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100 105 110

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Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
      115                      120                      125
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Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Thr Ala Ala
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys

180					185					190					
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Thr	Gln	Ser	Lys	Ile	Asp	Val	His	Arg	Lys	Glu	Asn	Ala	Gly	Ala	Ala
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Glu	Lys	Ser	Ile	Thr	Ile	Leu	Ser	Thr	Pro	Glu	Gly	Thr	Ser	Ala	Ala
				245					250					255	
Cys	Lys	Ser	Ile	Leu	Glu	Ile	Met	His	Lys	Glu	Ala	Gln	Asp	Ile	Lys
			260					265					270		
Phe	Thr	Glu	Glu	Ile	Pro	Leu	Lys	Ile	Leu	Ala	His	Asn	Asn	Phe	Val
	275						280					285			
Gly	Arg	Leu	Ile	Gly	Lys	Glu	Gly	Arg	Asn	Leu	Lys	Lys	Ile	Glu	Gln
	290					295					300				
Asp	Thr	Asp	Thr	Lys	Ile	Thr	Ile	Ser	Pro	Leu	Gln	Glu	Leu	Thr	Leu
	305				310				315						320
Tyr	Asn	Pro	Glu	Arg	Thr	Ile	Thr	Val	Lys	Gly	Asn	Val	Glu	Thr	Cys
				325				330						335	
Ala	Lys	Ala	Glu	Glu	Glu	Ile	Met	Lys	Lys	Ile	Arg	Glu	Ser	Tyr	Glu
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	355						360					365			
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	370					375					380				
Pro	Thr	Ser	Gly	Pro	Pro	Ser	Ala	Met	Thr	Pro	Pro	Tyr	Pro	Gln	Phe
	385				390				395						400
Glu	Gln	Ser	Glu	Thr	Glu	Thr	Val	His	Leu	Phe	Ile	Pro	Ala	Leu	Ser
				405				410						415	
Val	Gly	Ala	Ile	Ile	Gly	Lys	Gln	Gly	Gln	His	Ile	Lys	Gln	Leu	Ser
			420					425					430		
Arg	Phe	Ala	Gly	Ala	Ser	Ile	Lys	Ile	Ala	Pro	Ala	Glu	Ala	Pro	Asp
	435						440					445			
Ala	Lys	Val	Arg	Met	Val	Ile	Ile	Thr	Gly	Pro	Pro	Glu	Ala	Gln	Phe
	450					455					460				
Lys	Ala	Gln	Gly	Arg	Ile	Tyr	Gly	Lys	Ile	Lys	Glu	Glu	Asn	Phe	Val
	465				470				475					480	

Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
 485 490 495

Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
 500 505 510

Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
 515 520 525

Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
 530 535 540

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
 545 550 555 560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser
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Arg Arg Lys

<210> 349

<211> 207

<212> DNA

<213> Homo sapiens

<400> 349

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<210> 350

<211> 69

<212> PRT

<213> Homo sapiens

<400> 350

Met Trp Gln Pro Leu Phe Phe Lys Trp Leu Leu Ser Cys Cys Pro Gly
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Ser Ser Gln Ile Ala Ala Ala Ala Ser Thr Gln Pro Glu Asp Asp Ile
 20 25 30

Asn Thr Gln Arg Lys Lys Ser Gln Glu Lys Met Arg Glu Val Thr Asp
 35 40 45

Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His
 50 55 60

Gly Ala Asn Arg Phe
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